## STIC-Biotech/ChemLib

From:

Sent: To:

Ibrahim, Medina A. Tuesday, November 05, 2002 1:27 PM STIC-Biotech/ChemLib 09/771, 045

Subject:

## Please search the following:

1. SEQ ID NO:35

2. oligo search of at least 20 contiguous bases of SEQ ID NO:35. Please search both commercial and issued patents databases. Thanks

Medina A. Ibrahim Patent Examiner GAU:1638 CM1-9A12 mailbox-9E12 (703)306-5822

> POINT OF CONTACT: PAUL SCHULWITZ **TECHNICAL INFO. SPECIALIST** CM1 6B06 TEL. (703) 305-1954

	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher:	NA Sequences:/	STN:
Phone:	AA Sequences:	DIALOG:
Location:	Structures:	Questel/Orbit:
Date Picked Up: 1/7	Bibliographic:	DRLink:
Date Completed: ///Z	Litigation:	Lexis/Nexis:
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QY	1141	CGGTGTCCTCTCAGGTAGGGGACTCG	GTTTCTTAGTGG1 	TCATTCCAGG	GGTATGCAG7                    GGTATGCAG7	STCGATT	1200 1200
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Qy	1261	GGAATTGAGCAGTCGGCGTCCGGCTG	TGTATAGTACGATCGGO 	CGGCCTCGGG	1000000 11111 0000000	GTTCCGA          GTTCCGA	1320 1320
QY	1321	AGCAAAAAGGTGGTGGTTTCGTTACC 	GTTACCGACAACATTGTATCCCACCTTGA 	ATCCCACC	CATI	TTCACCA              TTCACCA	1380 1380
QY Db	1381	CCTCTTCCCGCCGAGAACAAGATTGGCGGAAAAACTATCCTCGGCTACTA'	'GGCGGAAAAT                 GGCGGAAAAT	CTATCCTC	GGCTACTAT	TAGCAAG         TAGCAAG	1440
QY	1441	ATAGTCTTCGTATGGGACAACCCGTGGTG	GTGGCGGAACAAGGC 	AAGGCTTC 	CTTCTCGGGCGTC	CCTCCAA          CCTCCAA	1500 1500
QY	1501	TCGAGCTGTGACCCCATCTCATTTGC	GCCAGAGATACCAGCATU 	GCATCGAA            GCATCGAA	rcgaagtcgatcgg                    rcgaagtcgatcgg	CAATGG         CAATGG	1560 1560
Qy	1561	TCCATTACCTGTTTCATGGTCGGAGACC	.cccgggacggaagtgg 	AGTGGTCC(             AGTGGTCC(	DAACAGTC	CAAGCAG 	1620 1620
Qy	1621	GTACGACAAAAGTCTGTGGGACCAACTC	ACTCCGCGCAGG 	CCTAC	GAGAACGCCGGG 	SGCCCAA 	1680 1680
QY	1681	GTCCCAGAGCCGGCCAACGTGCTCGA 	GAAATCGAGTGGT 	CGAAGCAGG              CGAAGCAGG	CAGTATIT	CCAAGGA               CCAAGGA	1740 1740
QY	1741	GCTCCGAGCGCCGTCTATGGGCTGAACGATC 	CGATCTCATCACACTG	CACTGGGT	rcssccr 	CAGAACG         CAGAACG	1800 1800
Qy	1801	CCGTTCAAGTGTGTTCATTTCGTTGG	GAACGGAGACGT 		rggaaagg          rggaaagg	STATATG         STATATG	1860 1860
QY	1861	GAAGGGCCATACGATCGGGTCAACG 	AGGTGCTGCAG1                 AGGTGCTGCAG2	aagttgtg          aagttgtg	GCTAGCCT              GCTAGCCT	GGTGCCA         GGTGCCA	1920 1920
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Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
Amino polyol amine oxidase polynucleotides
and methods of use
Patent: US 6211434-A 39 03-APR-2001;
Location/Qualifiers
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Matches 1887; Conservative
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                                                      CCTTATGGTGACTCCCCGGTAAGCACAATCCCACTTTGTGAGAGACCTCTGTCGAGTGT
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Pred. No. 0;
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Location/Qualifiers
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Duvick, J.P., Gilliam, J.T. a
Amino polyol amine oxidase
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AR145468
AR145468.1 GI:15107335
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Best Local Similarity 95.9
Matches 1850; Conservative
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Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
Amino polyol amine oxidase polynucleotides
and methods of use
Patent: US 6211434-A 41 03-APR-2001;
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AR145467.1 GI:15107334
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95.7%;
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Best Local Similarity 95.7
Matches 1847; Conservative
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Duvick J.P., Gilliam J.T. and Maddox, J.R.

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Patent: US 6211434-A 22 03-APR-2001;
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Best Local Similarity 91.7%;
Matches 1769; Conservative
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ACCESSION AR145484  KEYWORDS  SOURCE  ORGANISM  TITLE  AMTHORS  JOURNAL  AUTHORS  AU	Ouery Match  Ouery Match  B3.1%; Score 1602.6; DB 6; Length 1803;  Best Local Similarity 91.7%; Pred. No. 0;  Matches 1769; Conservative 0; Mismatches 34; Indels 126; Gaps 2;  Matches 1769; Conservative 0; Mismatches 34; Indels 126; Gaps 2;  A TAGGCACTTGCACCAGCTACATCATCACCAACGTCCCCCACCAGCGGTATTCC 60	181 CTGCGAGCTTGCTTGCTGCAGTTGGAGCTCTTTCAAACGACGTCCAGAGCTCAATTAC  181 CTGCGAGCTTGCTTGCAGTTGGAGCTCTTTCAAACGACGTCACCAAGCTCAATTAC  181 CTGCGAGCTTGCTTGCAGTTGGAGCCTCTTCAAACGACGTCACCAAGCTCAATTAC  181 CTGCGAGCTTGCTTGCAGTTGGAGCCTCTTCAAACGACGTCACCAAGCTCAATTAC  241 TACATCGTCGACTACGCCCCGAGCAAACTCGCCGAAATTGGAGATGGGCTGAAGTTAC  1111111111111111111111111111111111	421 GTTGCGGACGTGGTGGCGCTGGCTTGCCGGGACGCCCCCCCC	661 CTCCAGAGGACGGAAATTCAATCCATCAAGACGGTACAACCACTACAGCT 720
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polynucleotides
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Patent: US 6211434-A 32 03-APR-2001;
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Pred. No. 0;
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623 c 653 q
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Duvick,J.P., Gilliam,J.T. a
Amino polyol amine oxidase
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2242 1741 2302 1801 2362 1861 2422 1921 2482	E - HOOKER BEJ KK	source BASE COUNT ORIGIN OUERY MATCH Best Local s Matches 1765 OY 1 ATGG OY 1 ATGG OY 61 CACA OD 748 CACG	121 808 181 181 241 928 301 988 361
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ANTGACAGCAACCAAAGCGAAGTATCCAGATTGTTTGAAAGATTTCGTTTGGAGGGCGAG	GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACCT	CGGTGTCCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCATTCCAGGTAGGCGGCGGTTTCCAGGTAGGGTCGTTTCTAGTGGTCATTCCAGGTAGCAGTCGGTTTCCAGGTACCAGTAGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCATGCA	CCTCTTCCGGCCGAGAAGCATTGGCGGAAAATCTATCCTCGGCTACTATAGCAAGCA
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3ACAGG 3ACAGG 3ACAGG CAGAGG 111111 1ATGG1 1ATGG1 ATACAG	CCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TGTCC CATGC CATGC ATTGA ATTGA ATTGA AAAAA	CTTCC       
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1 (bases 1 to 2490)

1 (bases 1 to 2490)

Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O. Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use
and methods of use
Patent: US 6211415-A 32 03-APR-2001;

Location/Qualifiers 5 08-AUG-2001 1047 2421 420 120 180 867 240 927 300 987 360 807 Gaps 9 GCACTTGCACCGAGCTACATCCCCCAAACGTCGCCTCCCCAGCAGGGTATTCC SATCGGCGTAGGCCCAAACGAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA SCGAGCTTGCCTGCTGCAGTTGGAGCCTCTTCAAACGACGTCACCAAGCTCAATTAC ATCGTCGACTACGCCCCGAGCAAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC GCCCTTGACAGGCTCCCTCCTTGCACGCTGGTGCCAGTACCGGCCTTGGCTTCACCT VIACCICITIGAGGIIGAIGCCACGGCGCIGGIGCCAGGACACICGACCCCAGACAAC TICAAGTGTGTTCATTICGTTGGAACGCAGACGTCTTTAGTTTGGAAAGGCTATATG TTCAAGAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGGTATATG GGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCTCA PAT Length 2490; Indels linear . 9 38; ВВ DNA Score 1596.2; Pred. No. 0; 0; Mismatches 90 bp 1 6211435. 589 R145489 2490 equence 32 from patent US 62 R145489 GI:15107356 /organism="unknown" 623 c 653 g 82.7%; 91.5%; 5; Conservative GCATAG 1929 Similarity nknown

oy Og	421	1 GTTGCCGCACGTGGTAGTGGTGGCGCTGGCTTGAGCGGTTTGGAGACGGCACGCAAAGTC 480
δ	481	TGGATCGTAGGGGGAAAGACT 540
op	1168	CAGGCCGCCGGTCTGTCCTGCTTCTTGAGGCGATGGATCGTGTAGG
Qy	541	. CTGAGCGTACAATCGGGTCCCGGCAGGACTATCAACGACCTCGGCGCTGGGTGGATC 600
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Οy	721	CCTTATGGTGACTCCCCGGTAAGCACAATCCCACTTTGTGATGAGACCTCTGTCGAGTGT 78
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oy ob	781	AGAATACAGTCACTGACTCCAGCTGAGCGGAGGTTGCAAGTGCACTTGC 840
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δý	1021	
Ор	1635	AGCCACGAGATCAGCATGTTTTTTTCACCGACTACAAGAGCCACCGGTCTCAG 1694
οy	1081	TAATATTGTCTCGGACAAGAAGACGCCGGCAGTATATGCGATGCAAAACAGGTGCGTG 1140
qq	1695	TAATATTTTCTCGGACAAGAAGACGGGGGGGGGGATATGCGATG
οy	1141	CGGIGICCICTCAGGIAGGGGACICGIIICIIAGIGGICAIICCAGGIAIGCAGIICGAII 1200
Dp	1745	
Qy Db	1201	TGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAACACCCCGGCGCT 1260
δy	1261	132
Dp	1822	88
Oy Db	1321	13
<u>۸</u>	1381	GAGAAGCAAGCAAGCAAAAAAAAAAAAAAAAAAAAAAA
qq	94	
Οÿ	1441	ATAGTCTTCGTATGGGACAACAGCTGGCGCGAACAAGGTTCTCGGGCGTCCTCCAA 1500
Dβ	2002	ATAGTCTTCGTATGGGACAAGCCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTCCTCCAA 2061
Qγ	1501	TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGGCAATGG 1560
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Unclassified.

1 (bases 1 to 1442)

1 (bases 2 to 1422)

1 (bases 3 to 1422)

1 (bases 3 to 1442)

1 (bases 4 to 1211 to 1422)

2 Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use

Patent: US 6211434-A 7 03-APR-2001; 1; PAT 08-AUG-2001 2121 1800 2361 GAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA 1920 474 534 594 180 Gaps 9 TCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCCAAGCAG 1122 TCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCCAAGCAG GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGGCCCAA 2182 GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGCCCAA CCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGGTATATG 475 AAAGTCCAGGCCGCCGGTCTGTCCTGCCTCGTTCTTGAGGCGATGGATCGTGTAGGGGGA 535 AAGACTCTGAGCGTACAATCGGGTCCCGGCAGGACGACTATCAACGACCTCGGCGCTGCG 415 GACAACGTTGCGGACGTGGTAGTGGTGGGCGCTTGAGCGGTTTGGAGACGGCACGC 73; Length 1442; linear Indels 25; 9; DNA DB ı, 68.4%; Score 1319; D 93.5%; Pred. No. 0; Live 0; Mismatches AR145448 1442 bp Sequence 7 from patent US 6211434. AR145448 1GI:15107315 309 1. .1442 /organism="unknown" 381 c 416 q Location/Qualifiers 416 g Query Match 68.4 Best Local Similarity 93.5 Matches 1417; Conservative GCAGCATAG 1929 336 a . Unknown. Unknown. RESULT 11 AR145448 LOCUS DEFINITION source 2062 1561 ACCESSION VERSION KEYWORDS SOURCE ORGANISM BASE COUNT 1621 1801 2362 1861 2422 1921 2482 AUTHORS TITLE REFERENCE JOURNAL FEATURES ORIGIN 셤 δλ qq  $\overset{\circ}{\Delta}$ Q Qγ 셤 óγ d δ q Óγ P δ ò g δ g οy qq

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Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.
Amino polyol amine oxidase polynucleotides and related polypeptides
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                                          CAAGGAGCTCCGAGCGCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCCTC
                              AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
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Patent: US 6211435-A 7 03-APR-2001;
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Z E	AUTHORS DUVÍCK, J. P. TITLE Amino polyc and methods JOURNAL Patent: US FEATURES LC SOURCE L  BASE COUNT 564 a	IGIN  Query Match  Best Local Sim  Atches 1372;  409 ACCCCA	1582 469 1642 529	Oy 589 GCTGCGTGGATCA Oy 589 GCTGCGTGGATCA Db 1762 GCTGCGTGGATCA Oy 649 TTGGAGGCGAGC Db 1822 TTGGAGGCCGAGC	709	Db 1908		Qy 1069 CACCGGTCTCAGI
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Duvick,J.E., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O. Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use
Patent: US 6211435-A 26 03-APR-2001,

Unclassified.

AUTHORS TITLE REFERENCE

JOURNAL FEATURES

Location/Qualifiers

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                                                                                         GATCGGCAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAA
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Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
Amino polyol amine oxidase polynucleotides
and methods of use
Patent: US 6211434-A 24 03-APR-2001;
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November 12, 2002, 02:14:19; Search time 416 Seconds (without alignments) 10442.560 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                           OM nucleic - nucleic search, using sw model
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1929
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Exophiala spinifer	Exophiala spinifer	Exophiala spinifer	Rhinocladiella atr	Rhinocladiella atr	Rhinocladiella atr	Exophiala spinifer	DNA encoding a ful	DNA encoding GST-t
SUMMARIES	<u> </u>	AAZ58382	AAZ58383	AAZ58384	AAZ58386	AAZ58387	AAZ58385	AAZ58402		
	DB	21	21	21	21	21	21	21	21	21
	Query Match Length DB ID	1929	1929	1930	1928	1928	1928	1803	1803	2490
dР	Query Match							83.1		
	Score	1929	1925.8	1851.4	1792.2	1789	1787.4	1602.6	1602.6	1596.2
	Result No.	-	2	m	4	'n	9	7	α	σ

DNA encoding a fus	o poryor	encoding	encoaing	encoding	44	encoding	encoding	encoding	щ		o polyol	encoding	DNA encoding amino			encoding				DNA encoding an am	Exophiala spinifer	w	Exophiala spinifer	Nucleotide sequenc	Propionibacterium		n monoamine	Gene #2392 used to	adenoc	Lung cancer relate	Φ	Micrococcal putres	-		Drosophila melanod	•
AAZ6064	AA25839	-	AAZ5840					AAZ60645	AAZ5840				AAZ58401												_		-	-	-	ABL6627				ABL23641	ARI.1874	
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2490	1442	1442	2976	2976	3003	3003	3591	3591	3618	3618	1392	1392	1464	1464	1673	1673	2079	2079	1389	1389	372	372	182	182	66788	1619	2491	2491	2491	2491	2491	2386	1347	3559	3645	,
82.7	68.4	68.4	62.8	62.8	62.8	62.8	62.8	62.8	62.8	62.8	62.8	62.8	62.8	62.8				62.8	62.8	62.8	18.7	18.7	0.6	9.0	2.6	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.0	c	•
1596.2	1319	1319	1212.2	1212.2	1212.2	1212.2	1212.2	1212.2	1212.2	1212.2	1212	1212	1212	1212	1212	1212	1212	1212	1211	1211	361.4	361.4	174	174	49.2		0		0	0	0		0			
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## ALIGNMENTS

RESULT 1

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Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ds.
                                                       Exophiala spinifera amino polyol amine oxidase ESP002_C2 DNA.
                                                                                                                                    /*tag= a
/note= "contains introns"
739.811
/*tag= b
1134..1186
/*tag= c
                                                                                                                  Location/Qualifiers
1..1929
        AAZ58382 standard; DNA; 1929 BP.
                                                                                                                                                                                                                                                 98US-0092936.
                                                                                                                                                                                                                                99WO-US15454
                                         23-MAY-2000 (first entry)
                                                                                                   Exophiala spinifera.
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21-MAY-1999;
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AAZ58382
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                                                                                                                                                    New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed grain or in silage
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Pred. No. 0;
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Best Local Similarity 100.0%;
Matches 1929; Conservative C
              (PION-) PIONEER HI-BRED (CURA-) CURAGEN CORP.
                                                                 Gilliam JT,
                                                                                                 WPI; 2000-182425/16.
P-PSDB; AAY58900.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ds.
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The present sequence is that of an isolated nucleic acid, designated ESP00_2. G. of Exophiala spinifera isolate ESP002, c. designated ESP00_2. G. of Exophiala spinifera isolate ESP002, c. which encodes an amino pollyol amino oxidase (APAO, see AAY58901) capable of degrading fumonisin, its hydrolysis product API, and related mycotoxins. The DNA was obtained by PCR amplification of ESP002 mycelial DNA using primers based on APAO of E. spinifera ATCC 74269. The invention provides APAO polymucleotides (see AAX58383-87) and polypeptides (see AAX58900-05) of E. spinifera and Rhinocladialla atrovirens. The polymucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Transgenic plants can be regenerated from the transformed plant cells. Also provided are methods for expressing both APAO and a fumonisin-esterase in a transgenic plant, and for producing APAO enzyme in prokaryotic and non-plant eukaryotic systems. Transgenic plants capable of degrading fumonisin or of producing the degrading enzymes are provided. Methods for cops and cetoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed. APAO
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The present sequence is that of an isolated nucleic acid, designated ESP003_C12, of Exophiala spinifera isolate ESP002, which encodes an amino polyol amine oxidase (APAO, see AAY58902) capable of degrading fumonisin, its hydrolysis product API, and related mycotoxins. The DNA was obtained by PCR amplification of ESP003 mycelial DNA using primers based on AAPO of E. spinifera AAC 74269. The invention provides APAO polynuclectides (see AAX5883-87) and polypeptides (see AAX58900-05) of E. spinifera and Rhinocladiella atrovirens. The polynuclectides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Transgenic plants can be regenerated from the
                                                                                                                                                                                                                                                                                       Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ds.
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  CCGTTCAAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGGTATATG
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                                                                                                                                                                                                                                                                   Length 1930;
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transformed plant cells. Also provided are methods for express both APAO and a fumonishn-esterase in a transgenic plant, and producing APAO enzyme in prokaryotic and non-plant eukaryotic systems. Transgenic plants capable of degrading fumonish or producing the degrading enzymes are provided. Methods for detoxification of grain, grain processing, sliage, food crops in animal feed and rumen microorganisms are also disclosed. A polynucleotide is also useful as a selectable marker.
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Pred. No. 0;
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Best Local Similarity 97.8%;
Matches 1887; Conservative C
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The present sequence is that of an isolated nucleic acid, designated RAT011-C2, of Rhinocladiella atrovirens isolate RAT011, which encodes an amino polyol amine oxidase (APAO, see AAY58904) capable of degrading fumonisin, its hydrolysis product API, and related mycotoxins. The DNA was obtained by PCR amplification of RAT011 mycelial DNA using primers based on APAO polynucleotides (see AAC58383-87) and polypeptides (see AAX58900-05) of R. atrovirens and Exophiala spinifera. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for detecting and mycotoxin in processed
                                                                                                                                                           Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ds.
                                                                                                                            Rhinocladiella atrovirens amino polyol amine oxidase RAT011-C2 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fungus infection. Transgenic plants can be regenerated from the transformed plant cells. Also provided are methods for expressing both APAO and a fumonisin-esterase in a transgenic plant, and for producing APAO enzyme in prokaryotic and non-plant eukaryotic systems. Transgenic plants capable of degrading fumonisin or of producing the degrading enzymes are provided. Methods for detoxification of grain, grain processing, sliage, food crops and in animal feed and rumen microorganisms are also disclosed. APAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotides, polypeptides useful for degrading fumonisin or structurally related mycotoxin
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                                                                                              (first entry)
                                                                                                                                                                                                      Rhinocladiella atrovirens.
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21-MAY-1999;
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DB 21; Length 1928;

Score 1792.2; Pred. No. 0;

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Best Local Similarity

Query Match

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detoxification; animal feed; silage; selectable marker;
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P-PSDB; AAY58905.
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Matches 1848; Conserv
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        TAATATTGTCTCGGACAAGAAGACGGCGGCAGTATATGCGATGCAAAACAGGTGCGTG 1140
                                                                            TGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAACACCCCCGTCGCT 1260
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The present sequence is that of an isolated nucleic acid, casignated RAPO11-C4, of Rhinocladiella atrovirens isolate RAT011, which encodes an amino polyol amine oxidase (APAO, see AAY58905) capable of degrading fumonisin, its hydrolysis product API, and caracted mycotoxins. The DNA was obtained by PCR amplification of RAT011 mycelial DNA using primers based on APAO of E. spinifera ATCC 74269. The invention provides APAO polynucleotides (see CAA258383-87) and polypeptides (see AAY58900-05) of R. atrovirens and Exophiala spinifera. The polynucleotides are used to transformed plant cells normally susceptible to Fusarium or other toxin-producing transformed plant cells. Also provided are methods for expressing both APAO and a fumonish-esterase in a transgenic plant, and for green managenic plant enkaryotic and non-plant enkaryotic and managenic plant.
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                                                                       Location/Qualifiers
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silage; selectable marker; ds.
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                                                                                                                                                                                                                                                      The present sequence is that of an isolated nucleic acid, designated RAT011-C1, of Rhinocladiella atrovirens isolate RAT011, which encodes an amino polyol amine oxidase (APAO, see AAY5893) capable of degrading fumonisin, its hydrolysis product API, and related mycoctoxins. The DNA was obtained by PCR amplification of RAT011 mycelial DNA using primers based on APAO of E. spinifera ATCC 74269. The invention provides APAO polynucleotides (see AAY58930-05) of R. atrovirens and Exophiala spinifera. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing tungus infection. Transgenic plants can be regenerated from the transformed plant cells. Also provided are methods for expressing both APAO and a fumonish-esterase in a transgenic plant, and for systems. Transgenic plants can hor-plant eukaryotic systems. Transgenic plants capable of degrading fumonish or of producing the degrading enzymes are provided. Methods for cyps and in animal feed and rumen microorganisms are also disclosed. APAO plynucleotide is also useful as a selectable marker.
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                                                                                                                                                                                        ed polynucleotides, polypeptides useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1787.4;
Pred. No. 0;
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                                                                                                                                                                                                                                     Claim 1; Page 143-44; 154pp; English.
                                                                                                                                    Maddox JR;
                                                                                                 HI-BRED INT INC
                                                                                                                                                                                         New isolated polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.7%;
                                                                 98US-0092936
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                                            99WO-US15454
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WO200004159-A1
                                                                15-JUL-1998;
21-MAY-1999;
                                           08-JUL-1999;
                      27-JAN-2000
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                                                           GTTGCGGACGTGGTAGTGGTGGCCCTGGCTTGAGCGGTTTGGAGACGGCACGCAAAGTC
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GTCCCAGAGCCGCCAACGTGCTCGAATCGAGTGGAGGAGCAGTATTTCCAAGGA
                                                                                                                                       GTCCCAGAGCCGGCCAACGTGCTCGAGTCGAGTGGTCGAAGCAGCAGTATTTCCAAGGA
                                                                                                                                                                                                                       GAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCCTAGCCTGGTGCCA
                                  1500 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGGCAATGG
                                                         TCCATTACCTGTTTCATGGTCGGAGGACCGGGAGGGAGGTGGTCCCAACAGTCGAGCAG
                                                                 1560 TCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCCAAGCAG
                                                                                        GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGCCCAA
                                                                                                 1620 GTACGACAGAAGTCTGTGTGTGTGTGTCCGCGCAGCCTACGAGACGCCGGGGCCCAA
                                                                                                                                                        GCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACG
                                                                                                                                                                                       CCGTTCAAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGGTATATG
                        TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGGATCGGCAATGG
                                                                                                                                                                                                                                                                                                                                                              Exophiala spinifera amino polyol amine oxidase cDNA
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                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                                                              AAZ58402 standard; cDNA; 1803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0092936
99US-0135391
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P-PSDB; AAY58913.
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21-MAY-1999;
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The present sequence is that of the coding region of full-length amino polyol amine oxidase (APAO) CDNA of Exophiala spinifera 2141.10. APAO is capable of degrading fumonishin, its hydrolysis product API, and related mycotoxins. The invention provides APAO polynucleotides (see AAZ58383-87) and polypeptides (see AAY58900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Transgenic plants can be reconsisted from the transformed plant cells. Also provided are methods for expressing both APAO and a fumonishin esterase in a transgenic plant, and for producing APAO enzyme in prokaryotic and non-plant eukaryotic systems. Transgenic plants capable of degrading con-plant eukaryotic systems. Transgenic plants capable of degrading (monishin or of producing the degrading enzymes are provided. Methods for detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed. APAO polynucleotide is also useful as a selectable marker.
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Best Local Similarity 91.7%;
Matches 1769; Conservative
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1675 CCGTTCAAGAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGGTATATG 1734
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Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding aminopolyol amine oxidase, used, generate plants resistant to Fusarium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding a full length aminopolyol amine oxidase APAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in engineered bacteria and fungi, e.g. rumen microflora.
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ċ	S S	Ωy	qq	ΟŸ	qq	Oy	QQ	ογ	qq	δy	qa	δŏ	qq	OY Db	ΟŸ	QQ	Qy	QC	ΟŊ	QQ	ΟŊ	QQ	οy	qq	Oy	QQ	δλ	QQ		a X	XX	XX	XX KW KW
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	CAGCA	CAGCA	CACAG 1111		A					CCTTGC	CCTTG	CGACC	CGACCC	CGGCAC		1 HGGGG		CCCTC	ATTTGC	ATTTGG	CAACC	CAACCA	CCTCTC		GCAAGI	11111 3CAAG1	SAAGAC	CAAGAC	IGTGAG	rereac		SCCACC	SCCACO
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Qy Db	1081	TAATATTGTCTCGGACAAGAAGACGGCGGCAGTATATGCGATGCAAAACAGGTGCGTG 1140
QY	1141	CICAGGTAGGGGACTCGTTTCTTAGTGGTCATTCCAGGT
QQ	1058	ATGCAGTCGAT
Qy Db	1201	aaggaacttgttccaggctcagt 
Oy Db	1261 1135	GGAATTGAGCAGTCGGCGTCGGCTGTATAGTACGATCGGCCTCGGGCGCCCGTGTTCCGA 1320 
oy do	1321	AGCAAAAGGIGGIGGITTCGITACCGACAACAITGIAICCCACCTIGACAITITCACCA 1380 
QY	1381 1255	CCTCTTCCCGCCGAGAAGCAAGCATTGGCGGAAAATCTATCCTCGGCTACTATAGCAAG 1440 
Qy	1441	ATAGICTICGDAIGGGACAACCCGIGGIGGCGCGAACAAGGCITCTCGGGCGTCCTCCAA 1500
QY	1501	TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGGCAATGG 1560 
Qy Dp	1561	TCCATTACCTGTTTCATGGTCGGAGCCCGGACGGAAGTGGTCCCAACAGTCCAAGGG 1620
Qy	1621 1495	GTACGACAAAAGTCTGTCTGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGCCCAA 1680 
Qy	1681 1555	GTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTCCAAGGA 1740 
QY	1741	GCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACG 1800
Qy	1801	CCGTTCAAGTGTGTTCATTTCGTTGGAACGGAACGTCTTTAGTTTGGAAAGGTATATG 1860 
Qy Db	1861	GAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA 1920 
Qy dq	1921	GCAGCATAG 1929 
RES AAZ ID	ULT 9 58407 AAZ	407 standard;
X Y X	AAZ58	407;
E X	23-MA	Y-2000 (first entry)
K K X X	C C	polyol amine oxidase; APAO; fumonisi genic plant; detoxification; animal f
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GACGCTTCGGGCGTGACAGACCCTGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT CTGCGAGCTTGCCTTGCTGCAGTTGGAGCCTCTTCAAACGACGTCACCAAGCTCAATTAC 

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GACGCTTTGGGCGTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT

TITGCCCTTGACAGGCTCCCTCCTTGCACGCTGGTGCCAGTACCGGCCTTGGCTTCACCT 360

TACATCGTCGACTACGCCCCGAGCAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC 300

868

181

928

301

241

886

1048 421

361

1108

QQ

GAATACCTCTTTGAGGTTGATGCCACGGCGCTGGTGCCAGGACACTCGACCCCAGACAAC

GITGCGGACGTGGTAGTGGTGGCCGCTTGACCGGTTTGGAGACGCCACGCAAAGTC

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The present sequence is that of a polynucleotide encoding a GST.APAO fusion protein (see AAY58918) composed of glutathione S transferase and Exophiala spinifera amino polyol amino oxidase (APAO). 2 Codons of the APAO coding region have been altered by site-directed mutagenesis in order to change the glycosylation sterem of the fusion protein. These were the replacement of AAT (ASD) by TCC (Ser) at codon 430, and replacement of AAT (ASD) at codon 435. APAO is capable of degrading fumonisin and related mycotoxins. The invention provides APAO polynucleotides can and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other coxin-producing fungus infection. Also provided are methods for expressing APAO in transgenic plants, prokaryotic and non-plant cukaryotic systems. Methods for detexification of grain, grain processing, silage, food crops and in animal feed and rumen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detecting and in processed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2490;
selectable marker; glutathione S transferase; GST; mutant; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotides, polypeptides useful for degrading fumonisin or structurally related mycotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2490 BP; 625 A; 623 C; 653 G; 589 T; 0 other;
                                                                                                                                "gst fusion + polylinker"
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Pred. No. 0;
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                                                                                                                                                                                                        /*tag= c
/note= "extra lysine"
replace(1288..1290, TCC)
                                                                                                                                                                                                                                                                 replace(1303..1305, AAC)
                                                                                                                                                            /*tag= b
/product= "K:trAPAO"
                                                                               Location/Qualifiers
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microorganisms are also disclosed.
                           Chimeric - Schistosoma japonicum.
Chimeric - Exophiala spinifera.
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P-PSDB; AAY58918.
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21-MAY-1999;
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             1228 CIGAGCGIACAATCGGGICCCGGCAGGACGACIAICAACGACCICGGCGCGGGGTGGAIC 1287
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540
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 CAGGCCGCCGGTCTGTCCTGCCTTCTTGAGGCGATGGATCGTGTAGGGGGAAAGACT
                                               CTGAGCGTACAATCGGGTCCCGGCAGGACGACTATCAACGACCTCGGCGCTGCGTGGATC
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61 CACATCGGCGTAGGCCCAAACGAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120

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1 ATGGCACTTGCACCGAGCTACATCAATCCCCCAAACGTCGCCTCCCCAGCAGGGTATTCC 60

Pred. No. 0; ); Mismatches

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Similarity

Best Local Sim Matches 1765;

us-09-771-045a-35\_1.rng

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  CAGGTATGCAGTCGATT 1761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amine oxidase; APAO; mycotoxin degradation; antimicrobial; l invasion; hydrogen peroxide; Fusarium; fungi; ss.
                             AGCAAAAAGGTGGTGGTTTCGTTACCGACAACATTGTATCCCACCTTGACATTTTCACCA
                                                                                                       ATAGTCTTCGTATGGGACAAACCCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTCCTCCAA
                                                                                                                                                                                 1561 TCCATTACCTGTTTCATGGTCGGAGGCGGACGGAAGTGGTCCCAACAGCAG
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                                                         GGAATTGAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCCCTCGGGCGCCCGTGTTCCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding a fusion of GST/mutated aminopolyol amine oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Exophiala spinifera.
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2482 GCAGCATAG 2490
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The present sequence encodes a fusion protein of GST and a mutated Exophiala spinifera aminopolyol amine oxidase (APAO). The APAO protein has been mutated to remove potential glycosylation sites at postions 201 and 206. The APAO enzyme has homology to the flavin contraining amine oxidase family, that oxidise primary amine to an aldehyde or ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Contrainting on of mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins has paped generates, as a by-product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants own defensive systems. The APAO polyuucleotides are used to generate plants (particularly maize) that are resistant to Fusarium or other fungi that produce mycotoxins and/or to degrade such mycotoxins

CC (e.g. during ensilaging); for recombinant production of APAO polypeptides, as selection markers for plant transformation; and to isolate related sequences from other organisms. The APAO polypeptides

CC isolate related sequences from other organisms. The APAO polypeptides

In engineered bacteria and fungi, e.g. rumen microflora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       747
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                                                                                                                        the protein has been mutated to remove potential glycosylation sites at positions 201 and 206"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.7%; Score 1596.2; DB 21; Length 2490; 91.5%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding aminopolyol amine oxidase, used, e.g. generate plants resistant to Fusarium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                             Gilliam JT, Maddox JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2490 BP; 625 A; 623 C; 653 G; 589 T; 0 other;
                                                                    GST and a linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0;
0; Mismatches
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                                                                                                                     "aminopolyol
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                                                                /note= "encodes
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/*tag= a
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Matches 1765; Conservative
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                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP
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P-PSDB; AAY68854.
                                                                                                                                                                                                      WO200004160-A1.
                                  misc_feature
                                                                                                                                                                                                                                                                        08-JUL-1999;
                                                                                                                                                                                                                                                                                                           15-JUL-1998;
                                                                                                                                                                                                                                        27-JAN-2000
                                                                                    mat_peptide
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Db 1882 AGCAAAAAGGTGGTTTCGTTACCGACAACCTTGTATCCCACCTTGACATTTTCACCA 1941	OY 1381 CCTCTCCGCCGAGAAGCATTGGCGGAAAATCTATCCTGGCTACTATAGCAAG 1440	OY 1441 ATAGTCTTCGTATGGGACAACCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTCCTCCAA 1500 1511	QY 1501 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGGCAATGG 1560   16	OY 1561 TCCATTACCTGTTTCATGGTCGGAGACCGGGAGGGAAGTGGTCCCAACAGTCCAACAGG 1620	OY 1621 GTACGACAAAGTCTGTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGCCCAA 1680	OY 1681 GTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTCCAAGGA 1740	OY 1741 GCTCCGAGCGCCTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACG 1800	OY 1801 CCGTTCAAGTGTTCATTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGGTATATG 1860 	AY 1861 GAAGGGCCATACGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA 1920	Qy 1921 GCAGCATAG 1929             	RESULT 11 AA258393 ID AA258393 standard; cDNA; 1442 BP.	XX AC AAZ58393; XX DT 23-MAY-2000 (first entry)	Amino polyol amine oxidase truncated DNA k0n0-395_5.4. Amino polyol amine oxidase: fumonisin: mynotoxin: transments	KW detoxification; animal feed; silage; selectable marker; ss. XX OS Exophiala spinifera.	FH Key Location/Qualifiers FT CDS 1.1442 FT /*tag= a FT //ort= "Antains an intron"	FT intron 647699 FT XX XX WAYDANAMES-1	27-JAN-2000.	PF 08-JUL-1999; 99WO-US15454. XX PR 15-JUL-1998: 9RHS-0092936
241 TACATCGTCGACTACGCCCGGAGCAAACTCACGGCAATTGGAGATGGGCTGAAGTCTACC 300	TCACCT 								AGAATACAGTCACTGCCACTTCGTCCAGCTGAGCAGGTTGCAAGTGCACTTGC		901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACCT 960 	961 AAACTTGCCTGCTGTTCTCAGCGTGGCAACCAGATCACACGCGCTCTGCTCGGTGTGGA 1020 	1021 AGCCCACGAGATCAGCATGCTTTTTCTCACCGACTACATCAAGAGTGCCACCGGTCTCAG 1080 	GCGTG	CGATT	TCGCT	TCCGA	GAAATTGAGCAGTCGGCTGTGTACAGTACGATCGGCCTCGGGCGCGCGTGT AGCAAAAAGGTGGTGCTTTGGTTACCGACAACATGTATCCCACCTTGACATTTT

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AAZ60631 standard; DNA; 1442
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                                                                                                                                                                                                   The present sequence is that of polynucleotide k0n0-395_5.4, which encodes a truncated, but still functional, amino polyol amine oxidase (trApko-1, see AAY58907 and AAY58908). The polynucleotide was obtained by 3' and 5' RACE PCR using k0n0-395.5 (see AA258388), a partial APAO. CDNA of Exophiala spinifera. APAO is capable of degrading fumonisin, its hydrolysis product API and related myxocxins. The invention provides APAO polynucleotides (see AA258383-87) and polypeptides (see AA258900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Also provided are methods for expressing APAO in transgenic plants, prokaryotic and non-plant eukaryotic systems. Methods for edetoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed. APAO
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                                                                                                                             detecting and in processed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25; Indels
                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide can also be used as a selectable marker
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1442 BP; 336 A; 381 C; 416 G; 309 T; 0 other;
                                                                                                                             ced polynucleotides, polypeptides useful for
fumonisin or structurally related mycotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          68.4%; Score 1319; 93.5%; Pred. No. 0;
                                                                                                                                                                              Example 6; Page 77-79; 154pp; English
                                                               Maddox JR;
                         (PION-) PIONEER HI-BRED INT INC
99US-0135391
                                                                                      WPI; 2000-182425/16.
P-PSDB; AAY58907, AAY58908
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 93.5
Matches 1417; Conservative
                                                              Duvick JP, Gilliam JT,
                                     CORP.
                                                                                                                                                       grain or in silage
                                     CURAGEN
                                                                                                                              New isolated
21-MAY-1999;
                                                                                                                                           degrading
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                                                                                                                                                                                                                                                 468 GGAACTAAACTIGCCTGCTGTTCTCGGCGTAGCAAACCAGATCACACGCGCTCTGCTCGG
                                                                           TGTGGAAGCCCACGAGATCAGCATGCTTTTTCTCACCGACTACATCAAGAGTGCCACCGG
                                                                                                 1075 TCTCAGTAATATGTCTCGGACAAGAAGACGGCGGGCAGTATATGCGATGCAAAACAGG
                                                                                                                                                                        1315 TTCCGAAGCAAAAGGTGGTGGTTTCGTTACCGACAACATTGTATCCCACCTTGACATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1675 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC
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                                                                                                                                                                                                                                                                                                            TCGATTTGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAACACCCCC
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The present sequence encodes an Exophiala spinifera aminopolyol amine oxidase (APAO). The enzyme has homlology to the flavin containing amine oxidase family, that oxidise primary amine to an aldehyde or ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by-product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants own defensive systems. The APAO polynucleotides are used to generate plants (particularly maize) that are resistant to Fusarium or other fungithat produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related account of the programs of the APAO polypeptides are used to account the APAO plants of the APAO plants of the APAO plants are used to account the APAO plants of the APAO
                                                                                                                                                        Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial; plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding aminopolyol amine oxidase, used, e.g. generate plants resistant to Fusarium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi, e.g. rumen microflora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maddox JR
                                                                                                               DNA encoding an aminopolyol amine oxidase clone trAPAO-I.
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                                                                                                                                                                                                                                                                                                                                                "aminopolyol amine oxidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gilliam JT,
                                                                                                                                                                                                                                                                                                                                                                        'note= "contains an intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Page 78-80; 145pp; English.
                                                                                                                                                                                                                                                                               Location/Qualifiers
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93.5%;
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647..699
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700..1439
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                                                                                                                                                                                                                                 Exophiala spinifera.
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                                                                                                                                             TGGATCAATGACAGCAACCAAAGCGAAGTATCCAGATTGTTTGAAAGATTTCATTTGGAG
                                                                                                   715 ACAGCTCCTTATGGTGACTCCCCGGTAAGCACAATCCCACTTTGTGATGAGACCTCTGTC
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                                            AAGACTCTGAGCGTACAATCGGGTCCCGGCAGGACGACTATCAACGACCTCGGCGCTGCG
                                                                                                                                                                                                                        775 GAGTGTAGAATACAGTCACTGACTCCACTTCGTCCAGCTGAGCGAGGAGGTTGCAAGTGC
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73;

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Pred. No.

Best Local Similarity 93.5 Matches 1417; Conservative

415

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Length 1442;

GACAACGITGCGGACGIGGTAGIGGTGGCGCTGGCTTGAGCGGTTTGGAGACGCCACGC 474

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2000-182425/16.
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                                                                               1188 GCCCAAGTCCCAGAGCCGCCAACGTGCTCGAAATCGAGTGGTCGAGCAGCAGCAGTATTC
                                                                                                                                                                                     1368 TATATGGAAGGGCCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGGCTAACCTG
 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC
           1068 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACCC
                                            1128 AAGCAGGTACGACAAAAAGTCTGTCTGGGACCAACTCCGCGCGAGCCTACGAGAACGCCGGG
                                                                                                                  1248 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC
                                                                                                                                           AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
                                                                                                                                                                             1855 TATATGGAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG
                                                                                                                                                                                                                                                                                                                             DNA encoding fumonisin esterase-amino polyol amine oxidase fusion.
                                    AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG
                                                                      GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC
                                                                                                        CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC
                                                                                                                                                     Amino polyol amine oxidase; APAO; fumonisin esterase; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; barley; alpha-amylase; signal peptide; maize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/product= "fumonisin-esterase-K:trAPAO fusion"
73..75
                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "barley alpha-amylase signal
73..2973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= c
/note= "extra lysine codon"
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                           BP.
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                                                                                                                                                                                                                                                                                                                                                                                                 - Bacterium.
- Exophiala spinifera.
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99US-0135391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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21-MAY-1999;
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The present sequence is that of a polynucleotide encoding a fusion protein (see AAY58915) composed of the barley alpha-amylase signal peptide, and a bacterial fumorish esterase (BEST1) joined via a peptide linker to K:traPAPO (see AAY5809), a truncated, but functional, amino polyol amine oxidase of Exophiala spinifera. The construct was designed for expression and secretion in plants of a hybrid protein having BEST1 and APAO activity. The invention provides APAO polynucleotides (see AAX58383.87) and polypeptides (see AAY58900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin producing fungus infection. Also provided are methods for expressing APAO, optionally as a fusion protein with fumosinin esterase, in transgenic plants, chrokaryotic and non-plant eukaryotic systems. Methods for prokaryotic and non-plant eukaryotic systems. Methods for crops and in animal feed and rumen microorganisms are also disclosed.
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                                                ed polynucleotides, polypeptides useful for detecting and fumonisin or structurally related mycotoxin in processed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAGAAGGACCTAAAACTTGCCTGCTGTTCTCAGCGTGGCAAACCAGATCACACGCGCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 GCACGCAAAGICCAGGCCGCCGGICTGTCCTGCCTCGTTCTTGAGGCGATGGATCGTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2976 BP; 564 A; 932 C; 926 G; 554 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 90.2%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                      Example 13; Page 109-113; 154pp; English
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Matches 1372; Conserv
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P-PSDB; AAY58915
                                                         New isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGGGGCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAG 1728
                                                                                                                                                                                                                                      ACATTTTCACCACCTCTTCCCGCCGAGAAGCAAGCATTGGCGGAAAAATCTATCCTCGGC 1428
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                                                                                                                                                                                                                                                                               TACTATAGCAAGATAGTCTTCGTATGGGACAACCCGTGGTGGCGCGAACAAGGCTTCTCG
2169 CACCGGTCTCAGTAATATTTCTCGGACAAGAAAGACGGCGGCGCAGTATATGCGATGCAA
                                                                                                              ATGCAGTCGATTTGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAAC
                                                                                                                                                                GCCGTGTTCCGAAGCAAAAAGGTGGTTTTCGTTACCGACAACATTGTATCCCACCTTG
                                                                                                                                                                                                                                                GATCGGCAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAA
                                                                     AACAGGTGCGTGCGGTGTCCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCATTCCAGGT
                                                                                          -----CAGGT
                                                                                                                                  ATGCAGTCGATTTGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAAC
                                                                                                                                                      ACCCCCGTCGCTGGAATTGAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCCTCGGGC
                             AGCCTGGTGCCAGCATAG 2976
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The present sequence encodes a fusion protein of Exophiala spinifera aminopolyol amine oxidase (APAO) and a bacterial fumonisin esterase. The APAO enzyme has homilology to the flavin containing amine oxidase family, that oxidise primary amine to an aldehyde or ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by-product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants own defensive systems. The APAO polynoucleotides are used to generate plants (particularly maize) that are resistant to Fusarium or other fungi that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related sequences from other clasmins. The APAO polypeptides are used to degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi,
             Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Indels 126;
                                                                                                                                                          "aminopolyol amine oxidase/fumonisin
                                                                                                                                                                                                                                                                                                                                                                             /note= "the protein has an amino terminal Lys for optimized expression"
                                                                                                                                                                                                   /*tag= b
/note= "barley alpha amylase signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aminopolyol amine oxidase, used, to Fusarium -
                        plant fungal invasion; hydrogen peroxide; Fusarium; fungi; fumonisin esterase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maddox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2976 BP; 564 A; 932 C; 926 G; 554 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                "aminopolyol amine oxidase"
                                                                                                                                                                                                                                                                           /note= "bacterial fumonisin esterase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gilliam JT,
                                                                                                                                                                                                                                                            "fumonisin esterase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0;
0; Mismatches
                                                                                                                                                                        esterase fusion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1212.2;
                                                                                                                                                                                                                                                                                                                    /noté= "spacer sequence"
1585..2973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 103-108; 145pp; English.
                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PION-) PIONEER HI-BRED INT INC (CURA-) CURAGEN CORP.
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/product=
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generate plants resistant
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                                                                                                                                                          /product=
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Best Local Similarity 90.2
Matches 1372; Conservative
                                                                                                                                                                                                                                73..1545
                                                                                                                               .2976
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                                                                                                                                                                                                                                                                                        1546.
                                                                     Synthetic.
Exophiala spinifera.
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                                                                                                                                                                                                                                                                                          misc_feature
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DNA encoding a fusion of aminopolyol amine oxidase/fumonisin esterase.

(first entry)

16-MAY-2000

	1549	2596	0y 1609 CAGTCCAAGCAGGTA	Qy 1669 GCCGGGCCCAAGTC 	QY 1729 TATTCCAAGGAGCT	Qy 1789 GCGCTCAGAACGCCG		OY 1909 AGCTGGTGCACACA 	RESULT 15 AAZ58403 ID AAZ58403 standard; c	XX AZ S8403; XX DT 23-MAY-2000 (first	DNA encodi		Chimeric - Horde Chimeric - Exoph Kev	FT sig_peptide 1.77 FT **Target** FT mat_peptide 73	misc_feature		27-JAN-2000. 08-JUL-1999;	PR 15-JUL-1998; 98US-C PR 21-MAY-1999; 99US-C XX PA (PION-) PIONEER HI-BR PA (CURA-) CURAGEN CORP.	
409 ACCCCAGACAACGTTGCGGACGTGGTAGTGGTGGGCGCTTGGGCGGTTTGAGCGGTTTGGAGACG 468	1582 AGCAAAGACAACGTTGCGGACGTGGTAGTGGTGGCCGTTGGCGGTTTTGGAGACG 1641 469 GCACGCAAAGTCCAGGCCGCGGTCTGTCCTGCTCTTTGAGGCGATGGATG		529 GGGGGAAAGACTCTGAGCGTACAATCGGGTCCCGGCAGGACGACTATCAACGACCTCGGC 588 	589 GCTGCGTGGATCAATGACAGCAACCAAGCGAAGTATCCAGATTGTTTGAAAGATTTCAT 648 	649 TTGGAGGGGGAGCTCCAGAGGACGAGGAATTCAATCCATCAAGCACAGAGGGGTACA 708 		769 TCTGTCGAGTGTAGAATACAGTCACTGACTCCACTTCGTCCAGCTGAGCGAGGAGGTTGC 828 1908CTTGCTGAGGAGGAGTTGC 1928	829 AAGTGCACTTGCGGAACTCCTCCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTGA 888 	889 AGACCCCAAGGGGAGCCCTCAGGGGAAGCGGCTCGACAGTGTGAGCTTGGGGCACTACTG 948 	949 TGAGAAGGACCTAAACTTGCCTGCTGTTCTCAGCGTGGCAAACCAGATCACAGGCTCT 1008 	1009 GCTCGGTGTGGAAGCCCACGAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGC 1068 	1069 CACCGGTCTCAGTAATTGTCTCGGACAAGAAAGACGGCGGGGGGTTTATGCGATGCAA 1128 	1129 AACAGGTGCGTGCGTGTCCTCAGGTAGGGGACTCGTTTCTTAGTGGTCATTCCAGGT 1188 	1189 ATGCAGTCGATTTGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAAC 1248 	1249 ACCCCGTCGCTGGAATTGAGCAGTCGGCTCCGGCTGTATACTACGATCGGCCTCGGGC 1308 	1309 GCCGTGTTCCGAAGAAAAGGTGGTGTTCGTTACCGACAACATTGTATCCCACCTTG 1368 	1369 ACATTTCACCACCTCTTCCCGCGAGAAGCAAGCATTGGCGGAAAAATCTATCCTCGGC 1428 		409 GGCGICCICCAAICGAGCIGIGACCCCAICTCATITGCCAGAGAIACCAGCAICGAAGIC 1548
Qy	oy Oy	QQ	Oy Db	Qy Db	Qy Dp	Oy Op	Oy Ob	qa	oy .	Oy .	Cy da	Oy Db	Oy 1	0y 1	Oy 1 Db 2	0y 1 Db 2	Oy 1 Db 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

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ACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAAC 1668
                                                                                                                                                                CCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAG 1728
                                                                                                                                                                                                                        TCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCG 1788
                                                                                                                                                                                                                                                                                  GTTCAAGTGTGTTCATTCGTTGGAACGGAGACGTCTTTAGTTTGG 1848
                                             CATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAA 1608
                                                                                                                      AGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCT 1908
                                                                                                                                                                                                                                                                                                                                                              sin esterase-amino polyol amine oxidase fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxidase; APAO; fumonisin esterase; mycotoxin;
letoxification; animal feed; silage;
barley; alpha-amylase; signal peptide; maize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ag- a coduct= "barley alpha-amylase signal peptide" .3000 coduct= b coduct= "fumonisin-esterase-K:trAPAO fusion"
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te= "extra lysine codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ation/Qualifiers
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P.
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a spinifera.
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-0135391.
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                                                                                                                                                           The present sequence is that of a polynucleotide encoding a fusion protein (see AAY58914) composed of the barley alpha-amylase signal peptide, and Exophiala spinifera fumonistin esterase (ESP1) joined via a peptide linker to K:trAPAO (see AAY58909), a truncated, but functional, amino polyol amine oxidase of E. spinifera. The construct was designed for expression and secretion in plants of a hybrid protein having ESP1 and APAO activity. The invention provides APAO polynucleotides (see AAX58383-87) and polypeptides (see AAX58900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Also provided are methods for expressing APAO, optionally as a custom protein with fumosinin esterase, in transgenic plants, prokaryotic and non-plant eukaryotic systems. Methods for detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2015
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                                                                         detecting and in processed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGTCGAGTGTAGAATACAGTCACTGACTCCACTTCGTCCAGCTGAGCGAGGAGGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.8%; Score 1212.2; DB 21; Length 3003; ilarity 90.2%; Pred. No. 0; Conservative 0; Mismatches 23; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3003 BP; 690 A; 840 C; 819 G; 654 T; 0 other;
                                                                        ted polynucleotides, polypeptides useful for fumonisin or structurally related mycotoxin
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 Maddox JR;
 JI,
Gilliam
                            2000-182425/16
                                                                                                         in silage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                            P-PSDB; AAY58914
                                                                           isolated
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Matches 1372;
 JP,
                                                                                         degrading
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Duvick
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CAGTCCAAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGGGGGCGTACGAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGTGTTCCGAAGCAAAAAGGTGGTGTTTCGTTACCGACAACATTGTATCCCACCTTG
                                                                                                                                                                                                         TACTATAGCAAGATAGTCTTCGTATGGGACAACCCGTGGTGGCGCGGAACAAGGCTTCTCG
                                                                                                                                                                                                                                                                                      2503 TACTATAGCAAGATAGTCTTCGTATGGGACAAGCCGTGGTGGCGCGCGAACAGGCTTCTCG
                                                                                                                                                                                                                                                                                                                                                        GATCGGCAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                         2883 CAGTCCAAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCTAGAAAC
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GCTCGGTGTGGAAGCCCACGAGATCAGCATGCTTTTTCTCACCGACTACATCAAGAGTGC
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729 bp mRNA linear EST 08-MAR-2002 BJ375584 Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA clone ddc19a09 3', mRNA sequence.
BJ375584
BJ375584.1 GI:19284967
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 729)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Dictyostelium discoideum"
/strain="XXX"
/db_xref="taxon:44689"
/clone="ddc19a09"
                                                                                                                                                                                                                                                                                                                                                                                         Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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BJ375460
BJ431186
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Location/Qualifiers
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BJ377303 BJ373006
BJ377633 BJ377633
BJ431313 BJ431313
BJ374786 BJ374786
                                          2002, 02:21:50 ; Search time 2809 Seconds (without alignments) 11121.785 Million cell updates/sec
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      GenCore version
Copyright (c) 1993 - 2002
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Maximum Match 100%
Listing first 45 summaries
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BJ431313
BJ374786
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AU034174 AU034174 BJ430253 BJ430253 BM180292 daj87h11. BJ3774217 BJ374217 BJ377200 BJ377200

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1 (bases 1 to 742)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the aggregation
                                                                                                                            1244 TCAACACCCCGTCGCTGGAATTGAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCCT 1303
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/clone_lib="Dictyostelium discoideum cDNA library, CF"
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                                                                            Length 729;
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                                                                            Score 58.8; DB 13;
Pred. No. 1.5e-05;
                     /dev_stage="Culmination stage"
136 c 129 g 250 t
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/sex="mat A"
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Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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14.3%; Pred. No. 1.5e-05;
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142 c 132 q 252 t
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/organism="Dictyostelium
/strain="AX4"
/db_xref="taxon:44689"
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EST 08-MAR-2002
Dictyostelium
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1 (bases 1 to 730)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the culmination
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/clone="ddc25101"
/clone_lib="Dictyostelium discoideum cDNA library, CF"
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184 GTTGGTAGAATTCATTGGGCTGGTACAGAAACTGCTTCAGTTTGGATTGGTTATATGGAA 125
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                                                                                                       124 GGTGCCTTAGAATCAGGTTTTAGAGTTTCAAAAGAAATTAAAAGATA 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 57.4; DB 13;
Pred. No. 3.7e-05;
0; Mismatches 314;
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141 c 130 g 243 t
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Location/Qualifiers
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BJ377633.1 GI:19287016
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Matches 263;
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BJ377633/c
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/clone="ddc15e09"
/clone_lib="Dictyostelium discoideum cDNA library, CF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCGTTGGTTTCATTGCTGCTTCAGCCGCTAAAGATTGGGCTGAAAAATCACCAGAAGAA 356
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Dictyostelium discoideum.
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bass 1 to 711)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the
                                                               BJ373006 Tithear linear BJ373006 Dictyostelium discoideum cDNA library, CF discoideum cDNA clone ddc15e09 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                         1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshinigqenes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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130 c 121 g 240 t
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BJ373006.1 GI:19282389
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BJ431313 Dictyostelium discoideum cDNA library, VF Dictyostelium
discoideum cDNA clone ddv13p15 3', mRNA sequence.
                               1744 CCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCGTCAGAACGCCG 1803
                                                                                            1804 TTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGGTATATGGAA 1863
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1 (bases 1 to 610)
Urushihara, H., Tanaka, Y., Kohara, Y., and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the vegetative
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/sex="mat A"
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                                                   200 TATTTAGGTTACACTAGTCCAGGTACTCTACCAATGTGGTGAACATTNACGTGCTCCA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 TTATCTCCAAGAATCTTTTAGAGAAAAGTTGGAAAGAAGAAGAATATTCACGTGGTTGT 201
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Pred. No. 3.8e-05;
0; Mismatches 309; Indels
                                                                                                                                                           1864 GGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTA 1909
                                                                                                                                                                              'organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6856
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122 c 107 q 201
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/clone="ddv13p15"
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Location/Qualifiers
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BJ431313.1 GI:19406035
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BJ431313/C
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BJ374786 BJCtyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA clone ddc16407 3', mRNA sequence.
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1 (bases 1 to 611)

Urushihara, ... Tanaka, Y., Kohara, Y. and Shin-1, T.
Full length cDNa of Dictyostellum discoldeum at the culmination
1624 CGACAAAAGTCTGTCTGGGACCAACTCCGCGCGCGCTACGAGAACGCCGGGGCCCAAGTC 1683
                                                                                                                                                                                                                                                   1744 CCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACGCCG 1803
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/sex="mat A"
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                                             310 AGAAAGAGGCCGTCTTAGACTGTTATGCTCGTTGGT------GGGGTCCAAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                              139 GTTGGTAGAATTCATTGGCTGGTACAGAAACTGCTTCAGTTTGGATTGGTTATATGGAA
                                                                                                                           1684 CCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTCCAAGGAGCT
                                                                                                                                                                                  259 TTATCTCCAAGAATCTTTTAGAGAAAAGTTGGAAAGAAGAAGAAGAATATTCACGTGGTTGT
                                                                                                                                                                                                                                                                                                             199 TATTTAGGTTACACTAGTCCAGGTACTCTTACCAATGTGGTGAACATTTACGTGCTCCA
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Contact: Tadasus Ahin-i
Contact: Tadasus Ahin-i
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fai: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1864 GGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTT 1902
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ilarity 45.1%; Pred. No. 3.8e-05;
Conservative 0; Mismatches 313;
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125 c 113 g 192 t
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/db_xref="taxon:44689"
/clone="ddc16d07"
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Location/Qualifiers
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BJ374786.1 GI:19284169
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EST 10-MAR-2002
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Eurotact: Tadasu Shin.i

Contact: Tadasu Shin.i

Forter For Genetic Resource Information

National Institute of Genetics

1111 Yata.

Mishima.

Elso-81-6855

Email: tshinidgenes.ing.ac.jp.

Location/Qualifiers
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                                                            1444 GTCTTCGTATGGGACAACCCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTCCTCCAATCG 1503
                                                                                                                                           1504 AGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGCCAATGGTCC 1563
                                                                                                                                                                                                                           ATTACCTGTTTCATGGTCGGAGCCCGGGACGGAAGTGGTCCCAACAGTCCAAGGTAGTA 1623
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180 TATITIAGGITACACIAGICCAGGIACICICITACCAAIGIGGIGAACAITIACGIGCICCA 121
                                                                                                  471 ATCACCATCTATGATGAACCATTCTGGAGAAAAGAAGGTTATTCAGCTGAAGCCATCTCT 412
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                                                                                                                                                                                                                                                                                                                                             291 AGAAAGAGGCCGTCTTAGACTGTTATGCTCGTTGGT-----GGGGTCCAAAAGAA
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                                                                                                                                                                                  GATAAAGGTCCAATCTTTATCTGCTATGATGACTCTTCACATGACGATAAGAAAACAGCT
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Pred. No. 3.9e-05;
0; Mismatches 313;
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125 c 112 g 2
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/clone="dds5f18"
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Matches 264; Conservative
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BJ399347/C
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KEYWORDS
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                                                                                                                                                                                                                                                  1684 CCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTCCAAGGAGCT 1743
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Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 612)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the vegetative
  1504 AGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGCAATGGTCC 1563
                                                                                                                                                                   1624 CGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGCCCAAGTC 1683
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                                                                                   ATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCCAAGGGGTA
                                                                                                         121 GTTGGTAGAATTCATTGGGCTGGTACAGAAACTGCTTCAGTTTGGATTGGTATATGGAA
                                                                                                                                                                                                          292 AGAAAGAGAGCGGTCTTAGACTGTTATGCTCGTTGGT------GGGGTCCAAAAGCA
                           Length 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTA 1909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGTGCCTTAGAATCAGGTTTTAGAGTTTCAAAAGAAATTAAAGATA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2002)
Contact: Tadasu Shin-i
Conter For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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/organism="Dictyostelium discoideum"
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Pred. No. 3.8e-05;
0; Mismatches 313;
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/sex="mat A"
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125 c 113 g 194
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/clone="ddv1j21"
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Location/Qualifiers
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Unpublished (2002)
                                                                             Similarity
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                                                                    1384 CTTCCCGCCGAGAAGCAAGCATTGGCGGAAAAATCTATCCTCGGCTACTATAGCAAGATA 1443
                                                                                                                                                                                                                                                                                          1623
                                                                                                                                                                                                              1504 AGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGCAATGGTCC 1563
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1 (bases 1 to 648)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostellum discoideum at the culmination
AAAAAGGTGGTTTCGTTACCGACAACATTGTATCCCACCTTGACATTTTCACCACCT 1383
                                                                                                                                          1444 GICTICGIAIGGGACAACCCGIGGIGGCGCGAACAAGGCTICTCGGGCGTCCTCCAATCG 1503
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                                                                                              557 ATGCCACCAAGACGTGATGAACTCACTCAAAGAATGCCAATGGGTTCCGTCATTAAAACC 498
                                                                                                                                                                                                                                                                                                               377 ATCGTTGGTTTCATTGCTGCTTCAGCCGCTAAAGATTGGGCTGAAAAATCACCAGAAGAA 318
                                                                                                                                                                                                                                                  GATAAAGGTCCAATCTTTATCTGCTATGATGACTCTTCACATGACGATAAGAAAACAGCT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 TATITAGGITACACTAGICCAGGIACTCTCTACCAAIGIGGIGAACAITIACGIGCICCA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 GITGGIAGAATICATIGGGCTGGIACAGAACTGCTTCAGTTTGGTTATATGGAA 87
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/clone="ddc18m13"
/clone_lib="Dictyostelium discoideum cDNA library,
                  1564 ATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCAAGCAGGTA
                                                                                                                                                                                                                                                                                                                                                                                 L684 CCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTCCAAGGAGCT
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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Location/Qualifiers
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Dictyostelium discoideum
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                                                                                                                                                                                                                                                                                                                     626 AAATACATTGTTGCAATTCCACCAACATTGGCTGGCCGTATTCATTATTCACCATCT 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                               566 ATGCCACCAAGACGTGATGAACTCACTCAAAGAATGCCAATGGGTTCCGTCATTAAAACC 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               506 ATCACCATCTATGATGAACCATTCTGGAGAAAGAAGGTTATTCAGCTGAAGCCATCTCT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     446 GATAAAGGICCAATCTITATCTGCTATGATGACTCTTCACATGACGATAAGAAAACAGCT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 ATCGTTGGTTTCATTGCTGCTTCAGCCGTAAAGATTGGGCTGAAAAATCACCAGAAGAA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 AGAAAGAGCCGTCTTAGACTGTTATGCTCGTTGGT-----GGGGTCCAAAAGCA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 ITAICICCAAGAAICITITAGAGAAAGITGGAAAGAAGAAGAATAITCACGIGGITGI 216
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                                                                                                                                                                                                       6
                                                                                                                                       Length 648;
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 650)
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Fax: 81-559-81-6855
Email: tahinieqenes.nig.ac.jp.
Location/Qualifiers
                                                                                                                               Score 57.2; DB 13;
Pred. No. 3.9e-05;
0; Mismatches 313;
/dev_stage="Culmination stage" a 125 c 114 g 217 t
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Center For Genetic Resource Information
National Institute of Genetics
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BJ375565.1 GI:19284948
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ilarity 45.1%;
Conservative
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BJ430839 658 bp mRNA linear EST 13-MAR-2002 BJ430839 Dictyostelium discoideum cDNA library, VF Dictyostelium discoideum cDNA clone ddv9b03 3', mRNA sequence.
                                                                                                                                                         1. .651.
/organism="Dictyostelium discoideum"
/strain="AXA"
/db_xref="taxon:44689"
/clone="ddoilk04"
/clone=lib="Dictyostelium discoideum cDNA library, CF"
/sex="mat A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     454 GATAAAGGTCCAATCTTTATCTGCTATGACTCTTCACATGACGATAAGAAAACAGCT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 TATTTAGGTTACACTAGTCCAGGTACTCTCTACCAATGTGGGTGAACATTTACGTGCTCCA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 GTIGGTAGAATICATIGGGCIGGTACAGAAACIGCITCAGTITGGATIGGTATATGGAA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  634 AAATACATTGTTGCTAGTATTCCACCAACATTGGCTGGCCGTATTCATTATTCACCATCT 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           574 ATGCCACCAAGACGTGATGAACTCACTCAAGAATGCCAATGGGTTCCGTCATTAAAACC 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 GGTGCCTTAGAATCAGGTTTTAGAGTTTCAAAAGAAATTAAAGATA 58
                                       1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@qenes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.0%; Score 57.2; DB 13; Best Local Similarity 45.1%; Pred. No. 3.9e-05; Matches 264; Conservative 0; Mismatches 313;
                                                                                                                                                                                                                                                                                                                          /dev_stage="Culmination stage"
124 c 113 g 223 t
Center For Genetic Resource Information
National Institute of Genetics
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Dictyostelium discoideum
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BJ430839/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T. Full length cDNA of Dictyostellum discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                       1324 AAAAAGGTGGTGTTTCGTTACCGACAATTGTATCCCACCTTGACATTTTCACCACCT 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1384 CTTCCCGCCGAGAAGCAAGCATTGGCGGAAAAATCTATCCTCGGCTACTATAGCAAGATA 1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACACACTCCAAGCAGGTA 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGCCCAAGTC 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1684 CCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTCCAAGGAGCT 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1744 CCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACGCCG 1803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1804 TICAAGIGIGITCATITCGITGGAACGGAGCGICTITAGITIGGAAAGGGIATATGGAA 1863
         // clone="bictyostelium discoideum"
/strain="AX4"
/db.xref="taxon:44689"
/clone="ddc19m05"
/clone=lib="bictyostelium discoideum cDNA library, CF"
/sex="mat.A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 GTTGGTAGAATTCATTGGGCTGGTACAGAAACTGCTTCAGTTTGGATTGGTTATATGGAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 AGAAAGAGGCGTCTTAGACTGTTATGCTCGTTGGT------GGGGTCCAAAAGCA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          573 ATGCCACCAAGACGTGATGAACTCACTCAAAGAATGCCAATGGGTTCCGTCATTAAAACC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 AICGITGGITICALIGCIGCITCAGCCGCIAAAGAITGGGCIGAAAAAICACCAGAAGAA 334
                                                                                                                                                                                                                                                                                                                                                                                                 633 AAATACATTGTTGCAATTCCACCAACATTGGCTGGCCGTATTCATTATTCACCATCT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATAAAGGTCCAATCTTTATCTGCTATGATGACTCTTCACATGACGATAAGAAAACACT 394
                                                                                                                                                                                                                                                                                                           Gaps
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Dictyostelium discoideum
Bukaryota: Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 651)
                                                                                                                                                                                                                                                              Length
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Similarity 45.1%; Pred. No. 3.9e-05;
34; Conservative 0; Mismatches 313;
                                                                                                                                                              /dev_stage="Culmination stage"
124 c 113 g 221 t
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Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                           264:
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BJ374842 Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA clone ddc16b17 3', mRNA sequence.
                                                                                                                                    Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (Dassas 1 to 686)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="ddc16b17"
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/sex="mat A"
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                                                                                                                                                                                                                                                      Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6855 Email: tshini@qenes.nig.ac.in
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 3:0%; Score 57.2; DB 13; Similarity 44.1%; Pred. No. 4.1e-05; 94; Conservative 0; Mismatches 363;
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135 c 129 q 220 t
                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="AX4" /db_xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                              tshini@genes.nig.ac.jp
Location/Qualifiers
1..686
                                                                                                  Dictyostelium discoideum.
Dictyostelium discoideum
                                         BJ374842
BJ374842.1 GI:19284225
                                                                                                                                                                                                                              Unpublished (2002)
Contact: Tadasu Shin-i
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                                 Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the vegetative
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Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum
1 (bases 1 to 658)
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                                                                                    Unpublished (2002)
Contact: Tadasus Shin-i
Contact: Tadasus Shin-i
Contact: Tadasus Shin-i
Contact: Tadasus Mishima
Salilla Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
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/dev_stage="Growth phase'
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/db_xref="taxon:44689"
/clone="ddv9b03"
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Location/Qualifiers
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/clone="ddv2f15"
/clone_lib="blctyostelium discoideum cDNA library, VF"
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1 (bases I to 687)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostellum discoideum at the vegetative
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    GTGAACATTTACGTGCTCCAGTTGGTAGAATTCATTGGGCTGGTACAGAAAACTGCTTCAG 82
                                                                              81 TITGGATTGGTTATATGGAAGGTGCCTTAGAATCAGGTTTTAGAGTTTCAAAAGAAATTA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center For Genetic Resource Information
National Institute of Genetics
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/dev_stage="Growth phase"
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/organism="Dictyostelium
/strain="AX4"
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Location/Qualifiers
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Dictyostelium discoideum
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Eukaryota: 1 (bases 1 to 694)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the culmination
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/db_xref="taxon:44689"
/clone="ddc17n18"
/scone="hoctyostelium discoideum cDNA library, CF"
/sex="mat A"
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                                                 312 crgaaaarcaccagaagaagaagaagcgccrcrragacrgrrargcrcgrggg
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Contact: Tadasu Shin-i
Contert For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Dictyostelium discoideum"
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Location/Qualifiers
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1504 AGCIGTGACCCCATCTCATTGCCAGAGATACCAGCATCGAACGCAATGGTCC 1563
1564 ATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCCAAGCAGGTA 1623
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Search completed: November 12, 2002, 05:30:41 Job time: 2825 secs

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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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US-09-352-159-37

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US-09-352-159-41

US-09-352-159-32

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US-09-352-168-36

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US-09-352-168-16
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RESULT 1
US-09-352-159-35
Sequence 35, Application US/09352159A
Fatent No. 6211434
GENERAL INFORMATION:
APPLICANT: DUVICK, Jonathan P.
APPLICANT: GILIAM, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
CURREWF TILING DATE: 1999-07-12
EARLIER PILING DATE: 1999-07-12
EARLIER FILING DATE: 1999-07-25
EARLIER FILING DATE: 1999-07-25
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FRASEQ for Windows Version 3.0
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US-09-230-388-2

US-09-230-388-2

US-09-428-117-1

US-08-132-168A-31

US-08-132-168A-31

US-09-199-637A-366

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100.0%; Score 1929;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1929; Conservative 0; Mismatches
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ORGANISM: Exophiala spinifera
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LOCATION: (739)...(811)

NAME/KEY: intron

LOCATION: (1134)...(1186)

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GENERAL INFORMATION:
APPLICANT: DUVICK, Jonathan P.
APPLICANT: DUVICK, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynuclectides and Related Polypeptides and Methods of Use
TITLE OF INVENTION: Polynuclectides and Related Polypeptides and Methods of Use
TITLE OF INVENTION: DATE: 1999-07-12
CURRENT APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 46
SEQ ID NOS: 46
SEQ ID NO 37
EINGTHE FALLING DATE: 1999-05-21
EINGTHE FILING DATE: 1999-05-21
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ORGANISM: Exophiala spinifera
FEATURE:
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NAMB/KEY: intron
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Query Match  Query Match  Best Local Similarity 99.9%; Pred. No. 0;  Matches 1927; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Qy 1 ATGGCACTTGCACCGAGCTACATCCACCCCAAACGTCGCCTCCCCAGCAGGTATTCC 60	121 GACGCTTTGGCCGTGACAGCCCAGCCTACGAGAAACAGGTTGCCCAAGCATTGCCCAAT 18 121 GACGCTTTGGGCGTGACAGCCCAGCCTACGAGAAACAGGTTGCCCAAGCATTGCCCAAT 18 121 GACGCTTTGGGACAGACAGCCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 18 131 CTGCGAGCTTGCTGCTGCTGTTGGAGCCTCTTCAAACGACGTCACCAAGTTAC 24 111111111111111111111111111111111111	GTCTACC 30         GTCTACC 30 TTCACCT 36 	QY         361 GAATACCTCTTTGAGGTTGATGCCAGGGGCTGGTGCCAGGACCTCGACCCCAGACAAC         420           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	9 9 2	GGGCGAG          GGCCGAG TACAGCT	CCTTATGGTGACTCCCGGTAAGCACAATCCCACTTTGGATGAGACCTCTGTCCAGGTT	QY         84.1 GGAACTCCCCCGTATGGTCTCAGCTGATGAGATATAGCCTTGAAGACCCCAAGGC         90.0           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Pol
FILE REFERENCE: 1136
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER PLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE: 1998-05-21
EARLIER FILING DATE: 1998-05-21
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EARLIER FILING DATE: 1999-05-21
SOFTWARE: FastEED for Windows Version 3.0
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96.0%; Score 1851.4;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1887; Conservative 0; Mismatches
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ORGANISM: Exophiala spinifera
FEATURE:
NAME/KEY: intron
LOCATION: (739)...(811)
NAME/KEY: intron
LOCATION: (1134)...(1187)
NAME/KEY: misc_feature
LOCATION: (648)...(648)
OTHER INFORMATION: n = A,T,C or
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                                       CCTTATGGTGACTCCCCGGTAAGCACAATCCCACTTTGTGATGAGACCTCTGTCGAGTGT
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APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polynuclecting APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE: 1998-07-25
SARLIER FILING DATE: 1998-05-21
NUMBER: OF SQL ID NOS: 46
SOFTWARE: FASTERO for Windows Version 3.0
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                             Sequence 43, Application US/09352159A Patent No. 6211434 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Rhinocladiella atrovirens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.98;
95.98;
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Best Local Similarity 95.9
Matches 1850; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: intron
LOCATION: (739)...(811)
NAME/KEY: intron
LCCATION: (1134)...(1186)
                                                                                                                                            AGCAGCATAG 1930
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                                                                                                                                                                                                    US-09-352-159-43
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 43
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            GTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTCCAAGGA
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1800 CCGTTCAAGGGTGTTCATTTCGTTGGAACGGAGACGTCTTTGGTTTGGAAAGGGTATATG
                                         TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGGCAATGG
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APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Mandox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynuclectides and Related Pol;
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
EARLIER FILING DATE: 1999-05-21
SARLIER FILING DATE: 1999-05-21
NUMBER OF SEC ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
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95.8%; Pred. No. 0;
Live 0; Mismatches
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ORGANISM: Rhinocladiella atrovirens
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Matches 1848; Conserv
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US-09-352-159-45
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                                                                                                                                                 DB 4;
                                                                                                                                                                  81;
                                                                                                                                               92.7%; Score 1787.4;
95.7%; Pred. No. 0;
tive 0; Mismatches
                               3.0
   60/135,391
                               Version
                                                             TYPE: DNA ORGANISM: Rhinocladiella atrovirens
EARLIER APPLICATION NUMBER: 60/
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASTSEQ FOR WINDOWS VE
SEQ ID NO 41
                                                                                                                                                          Best Local Similarity 95.7
Matches 1847; Conservative
                                                                                                           NAME/KEY: intron
LOCATION: (1134)...(1185)
09-352-159-41
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LOCATION: (739).
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                                                                                                     ATAGTCTTCGTATGGGACAACCCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTCCTCCAA
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                                                               CCTCTTCCCGCCGAGAAGCAAGCATTGGCGGAAAAATCTATCCTCGGCTACTATAGCAAG
                CGGTGTCCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCATTCCAGGTATGCAGTCGATT
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Patent No. 6211434
GENERAL INFORMATION:
APPLICANT: Dilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Polynuclectides and Related Pol;
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
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US-09-352-159-41
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Matches 1769; Conserv
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LOCATION: (1)
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GRNERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Polyol Amine Oxidase
FITLE OF INVENTION: Polyouclectides and Related Pol;
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: 05/09/352,159A
CURRENT APPLICATION NUMBER: 06/092,936
EARLIER APPLICATION NUMBER: 60/1936
EARLIER FILING DATE: 1999-07-12
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 1803
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Sequence 22, Application US/09352168A

Patent No. 6211435

GENERAL INFORMATION:
APPLICANT: Crasta, Oswald R.
APPLICANT: DUVICK, Jonathan P.
APPLICANT: Folkerts, Otto
APPLICANT: Maddown Jacob T.
APPLICANT: Maddown Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Pol;
FILE REFERENCE: 10975
CURRENT APLICATION NUMBER: US/09/352,168A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/092,936
SECTION ON STANDAME: FASSEQ FOR Windows Version 3.0
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 91.7%;
Matches 1769; Conservative (
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APPLICANT: DUVICK, Jonathan P.
APPLICANT: Bulliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynclectides and Related Polypeptides and Meth
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER PILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 2490
                                                                                                                                          TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGGCAATGG
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Pred. No. 0;
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ilarity 91.5%;
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OTHER INFORMATION: mutation
FEATURE:
NAME/KEY: mutation
LOCATION: (1303)...(1305)
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NAME/KEY: CDS
LOCATION: (1)...(2487)
NAME/KEY: misc_feature
LOCATION: (1)...(687)
OTHER INFORMATION: GST and
FEATURE:
LOCATION: (688)...(2490)
OTHER INFORMATION: Glyc (-
FEATURE:
NAME/KEY: misc_feature
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                                                                                                                 AAACTTGCCTGCTGTTCTCAGCGTGGCAAACCAGATCACACGCGCTCTGCTCGGTGTGGA
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                                               ----CTTGCTGAGCGAGGAGGTTGCAAGTGCACTTGC
                               AGAATACAGTCACTGCACTTCGTCCAGCTGAGCGAGGAGGTTGCAAGTGCACTTGC
                                                                                                  GGAACTCCTCCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC
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APPLICANT: Divick, Jonathan P.
APPLICANT: Divick, Jonathan P.
APPLICANT: Divick, Jonathan P.
APPLICANT: Folkerts, Outo
APPLICANT: Folkerts, Outo
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
CURRENT FPLING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APLICATION NUMBER: 60/092,936
SOFTHARE: FastEGO ID NOS: 33
SOFTHARE: FastEGO for Windows Version 3.0
SSOTING OF SECTION OF SECTION
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OTHER INFORMATION: and linker, nt 1-687; Glyc (-) APAO, nt 688-2490;
OTHER INFORMATION: mutation in putative glycosylation sites in bold
OTHER INFORMATION: mutation in putative glycosylation sites in bold
OTHER INFORMATION: 1303-1305 (AGC-> AAC).
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(687)
NAME/KEY: misc_feature
LOCATION: (1)...(687)
NAME/KEY: misc_feature
LOCATION: (688)...(2490)
OTHER INFORMATION: GST and linker
FEATURE:
NAME/KEY: misc_feature
COCATION: (1)...(687)
OTHER INFORMATION: GST and linker
FEATURE:
RAME/KEY: misc_feature
COCATION: (2490)
OTHER INFORMATION: Glyc (-) APAO
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; OTHER INFORMATION: mutation in putative glycosylation site (AGC->AAC)
US-09-352-168-32
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OTHER INFORMATION: mutation in putative glycosylation site (AAT->TCC)
                                           2422 GAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA
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GACGCTTCGGGCGTGACAGACCCTGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 867
                                                                                                                                TACATCGTCGACTACGCCCCGAGCAAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC
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                                                                                             Score 1319; Di
Pred. No. 0;
0; Mismatches
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                                                                                              68.4%;
93.5%;
         ; LOCATION: (1)...(646)
; NAME/KEY: intron
; LOCATION: (647)...(699)
; NAME/KEY: CDS
; LOCATION: (700)...(1439)
US-09-352-159-7
                                                                                                                       Conservative
                                                                                                           Similarity
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NAME/KEY:
                                                                                                Query Match
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            GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGCCCAA
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                                                                                                CCTCTTCCCGCCGAGAAGCAAGCATTGGCGGAAAAATCTATCCTCGGCTACTATAGCAAG
                                                                                                              ATAGTCTTCGTATGGGACAACCCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTCCTCCAA
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 GGAATTGAGCAGTCGGCGTGTATAGTACGATCGGCCTCGGGCGCGTGTTCCGA
                                                 AGCAAAAAGGTGGTGGTTTCGTTACCGACATTGTATCCCACCTTGACATTTTCACCA
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APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polyouclectides and Related Poly
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-07-12
EARLIER FILING DATE: 1999-07-12
SALIER FILING DATE: 1999-07-12
SALIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: DNA
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                                                      Score 1319;
Pred. No. 0;
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                                                    68.4%;
93.5%;
                                                                          Matches 1417; Conservative
                  ; LOCATION: (700)...(1439)
US-09-352-168-7
                                                                Similarity
        NAME/KEY: CDS
                                                    Query Match
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Patent No. 6211435
GENERAL INFORMATION:
APPLICANT: Crasta, Oswald R.
APPLICANT: Polkerts, Otto
APPLICANT: Polkerts, Otto
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of US
FILE REFERENCE: 0875
CURRENT FILING DATE: 1999-07-12
EARLIER FILING DATE: 1999-07-12
EARLIER FILING DATE: 1999-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
1494
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                                                                                         AGCAAGATAGTCTTCGTATGGGACAACCCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTC
                                                                                                      TCACCACCTCTTCCCGCCGAGAAGCAAGCATTGGCGGAAAAATCTATCCTCGGCTACTAT
                                                         CTCCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGA
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NAME/KEY: intron
LOCATION: (647)...(699)
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US-09-352-168-7
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TYPE: DNA
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                    LOCATION: (1)...(2973)
WAME/KFX: misc.feature
LOCATION: (1585)...(1587)
OTHER INFORMATION: Extra lysine
               mature
                                                                                                                                                                                                                                                           62.8%;
90.2%;
                                                                                               NAME/KEY: misc_feature
LOCATION: (1585)...(2973)
OTHER INFORMATION: K:trAPAO
                                                     LOCATION: (1546)...(1584)
OTHER INFORMATION: spacer
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ION: (73)...(1545)
INFORMATION: BEST1
                                         misc_feature (1546)...(15
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                                                                                                                                                        NAME/KEY: CDS
LOCATION: (1)
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Matches 1372;
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            OTHER INFORESTANDEN
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APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polyouclectides and Related Polypeptides and Methods of Use
TITLE OF INVENTION: Polyouclectides and Related Polypeptides on Use
TITLE OF INVENTION: Polyouclectides and Related Polypeptides on Use
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER FILING DATE: 1999-07-25
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
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OTHER INFORMATION: Barley alpha amylase signal sequence: BEST1
OTHER INFORMATION: mature: artificial spacer: and K:trAPAO. F
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OTHER INFORMATION: Barley alpha amylase signal sequence
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Patent No. 6211434
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; LOCATION: (1)...(2973)
; NAME/REY: misc_feature
; LOCATION: (1585)...(1587)
; OTHER INFORMATION: Extra lysine
US-09-352-168-26
                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1585)...(2973)
OTHER INFORMATION: K:trAPAO
                                                                                                                      LOCATION: (1)...(72)
OTHER INFORMATION: Barley
FEATURE:
                                                                                                                 NAME/KEY: sig_peptide
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                         TYPE: DNA
ORGANISM: Unknown
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LOCATION: (1)
SEQ ID NO 26
LENGTH: 2976
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Matches 1372;
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Fatent No. 6211435

GENERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Buvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Polynclectides and Related Polypeptides and Methods of US;
TITLE OF INVENTION: Polynclectides and Related Polypeptides and Methods of US;
TITLE OF INVENTION: Polynclectides and Related Polypeptides of US;
TITLE OF INVENTION: Polynclectides and Related Polypeptides and Methods of US;
TITLE OF INVENTION: 1999-07-12

CURRENT APPLICATION NUMBER: 05/092,936

SARLIER APPLICATION NUMBER: 60/092,936

EARLIER FILING DATE: 1998-07-25

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 3.0
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                    ATGCAGTCGATTGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAAC
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OTHER INFORMATION: Barley alpha amylase signal sequence: BEST1 OTHER INFORMATION: mature: artificial spacer: and K:trAPAO. For OTHER INFORMATION: plant expression.
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                                                                                                                    alpha amylase signal sequence
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                                                                                                                                             LOCATION: (73)...(1545)
OTHER INFORMATION: BESTI mature
FEATURE:
FEATURE:
LOCATION: (1546)...(1584)
OTHER INFORMATION: Artificial spacer sequence
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ilarity 90.2%; Pred. No. 0;
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             2536 GGCGTCCTCCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAGCTC
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                                                                                                                                                                                                                                            2296 ACCCCGGTCGCTGAAATTGAGCAGTCGGCATCCGGCTGTACAGTACGGCCTCGGGC
                                                                                                                                                                                                                                                                                                ACATITICACCACCICITCCCGCCGAGAAGCAAGCATIGGCGGAAAAATCTATCCTCGGC
                                                                                                                                                                                                                                                                                                                                               TACTATAGCAAGATAGTCTTCGTATGGGACAACCCGTGGCGCGCGAACAAGGCTTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCGTCCTCCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTC
                                                                                  CACCGGTCTCAGTAATATTGTCTCGGACAAGAAGACGGCGGCGGCAGTATATGCGATGCAA
                                                                                              ATGCAGTCGATTTGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAAC
                                                                                                                                                                                                                                 ACCCCCGTCGCTGGAATTGAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCCTCGGGC
GCTCGGTGTGGAAGCCCACGAGATCAGCATGCTTTTTCTCACCGACTACATCAAGAGTGC
                                              -----CAGGT
                                                                                                                                 AACAGGTGCGTGCGCTCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCATTCCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-352-159-24; Sequence 24, Application US/09352159A; Patent No. 6211434; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2956 AGCCTGGTGCCAGCATAG 2976
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APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polyoucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE: 1999-05-21
SARLIER FILING DATE: 1999-05-21
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                       Use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           709 ACCACTACAGCTCCTTATGGTGACTCCCGGTAAGCACAATCCCACTTTGTGATGAGACC 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCCCAGACAACGTTGCGGACGTGGTAGTGGTGGCGCTTGGCCGTTTGAGCGGTTTGGAGACG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCACGCAAAGICCAGGCCGCCGGICIGICCIGCCICGTICTIGAGGCGAIGGAICGIGIA 528
                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Sequence is barley alpha amylase signal sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGCGTGGATCAATGACAGCAACCAAAGCGAAGTATCCAGATTGTTTGAAAGATTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGGAAAGACTCTGAGCGTACAATCGGGTCCCGGCAGGACGACTATCAACGACCTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 3003;
                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6211434
OTHER INFORMATION: espl mat: an artificial spacer sequence
OTHER INFORMATION: K:trAPAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COTHER INFORMATION: Barley alpha amylase signal sequence FEATURE:
NAME/FEX: misc_feature
LOCATION: (73)...(1575)
OTHER INFORMATION: espl mat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
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Pred. No. 0;
0; Mismatches
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; LOCATION: (1612)...(1614)
; CTHER INFORMATION: Extra lysine
US-09-352-159-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.8%;
90.2%;
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NAME/KEY: misc_feature
NCATION: (1612)...(3000)
OTHER INFORMATION: K:traPAO
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Best Local Similarity 90.2's
Matches 1372; Conservative
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LOCATION: (1576)...(1611)
OTHER INFORMATION: spacer
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                                                                                                                                                                                                                                                                                                                        LENGTH: 3003
TYPE: DNA
ORGANISM: Unknown
FEATURE:
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CCAGCTGAGCGAGGA 	TCACCGACTACATCA TCACCGACTACATCA TCACCGACTACATCAT TCACCGACTATATGCG GCGGCAGTATATGCG 11   1   1   1   1   1   1   1   1   1		ITTGCCAGAGATACCAGCATCGAA	AACGATCTCATCACGCGGIIIIIIIIIIIIIIIIIIIIII
CGTGACTC   CGTGACTC   CGTCACTGACTCCAC   CGTCCCCGTATGGTCT	CGGGATCAGCATGCTTTT	GAGCAGTCGGCGTCCGGC	GTGACCCCATCATTT	CGAGGGCGTCFATGGGCTG [
ACCACTACAGCTCCTTATC TCTGTCGAGTGTAGAATAC AAGTGCACTTGCGGAACTC AAGTGCACTTGCGGAACTC AAGTGCACTTGCGGAACTC AAGTGCACTTGCGGAACTC TGAGAACTC TGAGAACGCCTAAACTTC TGAGAACGACCTAAACTTC TGAGAACGACCTAAACTTC TGAGAACGACCTAAACTTC TGAGAAACTTC	CTCGGTGGG TCTCGGTGGG TCTCGGTGTGG ACCGGTCTCAC TILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	CCCCGTCGCTCG 	GGCGTCCTCCAATCGAGCT GGCGTCCTCCAATCGAGT GGCGTCCTCCAATCGAGT GATCGCAATGGTCCATTA GATCGCAATGGTCCATTA CAGTCCAAGCAGGTACGAC CAGTCCAAGCAGGTACGAC GCGCGGGCCCAAGTACGAG GCCGGGGCCCAAGTACGAG GCCGGGGCCCAAGTCCCAG GCCGGGCCCCAAGTCCCAG	TATTCCAAGGAGCTC                TATTTCCAAGGAGCTC GCGCTCAGAACGCCGT
1909 769 1935 829 1956 889 2016	136 136 1069 1129 129 256 263	49 69 69 7 69 03	1489 2563 1549 2623 1609 2683 1669	1729 2803 1789 2863
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Oy 1849 AAAGGTATATGGAAGGGCCATACGGTCAACGAGGTGCTGCAGAAGTTGTGGCT 1908

Db 2923 AAAGGTATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCT 2982

Qy 1909 AGCCTGGTGCCAGCAGAAG 1929

Db 2983 AGCCTGGTGCCAGCAGATAG 3003

Search completed: November 12, 2002, 05:32:16

Job time: 96 secs
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November 12, 2002, 03:21:40; Search time 140 Seconds (without alignments) 4888.437 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*/
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320260 seqs, 177392727 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                   - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                         IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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1929
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                                                                                                                                                                                                                                                                                            Title:
Perfect :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

					CHAMMA	
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Result		Query				
NO.	Score	Match	Length DB		QI	Description
1	40.8	2.1	2491	10	US-09-954-456-1583	Sequence 1583, Ap
7	40.8	2.1	2491	10	US-09-880-107-2391	Sequence 2391, Ap
m	39	2.0	2389	10	US-09-917-800A-1612	Sequence 1612, Ap
O 4	38	2.0	1386	10	US-09-925-301-562	Sequence 562, App
S	37.6	1.9	1095	10	US-09-974-300-239	Seguence 239, App
9	37.2	1.9	314	10	US-09-960-352-3971	Sequence 3971, Ap
7	36.6	1.9	1575	10	US-09-912-176-2	Sequence 2, Appli
80 ن	35.2	1.8	3276	10	US-09-925-302-242	Sequence 242, App
σ	34.8	1.8	1949	10	US-09-880-107-2388	Sequence 2388, Ap
10	34.8	1.8	3147	10	US-09-925-300-617	Sequence 617, App
11	34.8	1.8	4024	12	US-10-044-090-86	Sequence 86, Appl
12	34	1.8	2018	10	US-09-925-301-376	Seguence 376, App
13	34	1.8	2068	10	US-09-880-107-1744	
14	34	1.8	3370	12	US-10-044-090-339	Sequence 339, App
15	33.8	1.8	401	10	US-09-795-668-1008	Seguence 1008, Ap
16	33.8	1.8	401	10	US-09-795-686-1008	Sequence 1008, Ap
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19	33.8	1.8	1503841	10	US-09-795-686-1	Sequence 1, Appli

20 33.6 1.7 3708 10 US-09-904-065-7 c 21 33.4 1.7 413 10 US-09-50-288-466-947 c 23 33.2 1.7 351 10 US-09-50-863-412 c 23 33.2 1.7 3033 9 US-09-50-880-410-1765 c 24 33 1.7 3056 10 US-09-974-298-80 c 26 32.8 1.7 443 9 US-10-046-935-1599 c 26 32.8 1.7 465 10 US-09-880-170-1765 c 29 32.8 1.7 269 10 US-09-867-770-15341 c 29 32.8 1.7 269 10 US-09-867-770-149 c 29 32.8 1.7 269 10 US-09-867-770-149 c 30 32.4 1.7 1557 10 US-09-867-280-3 3 32 1.7 1557 10 US-09-861-289-13 c 33 32 1.7 1557 10 US-09-861-289-15 35 32 1.7 13029 10 US-09-961-289-15 35 32 1.7 13029 10 US-09-961-289-15 35 32 1.7 13029 10 US-09-961-289-15 35 31.8 1.6 420 10 US-09-811-289-15 c 34 31.8 1.6 420 10 US-09-811-289-15 44 30.8 1.6 442 10 US-09-181-28-31 1.6 442 10 US-09-181-2-8018 44 30.8 1.6 442 10 US-09-764-878-391
20 33.6 1.7 3708 10 22 33.4 1.7 413 10 23 33.4 1.7 413 10 24 33.8 1.7 3033 9 25 32.8 1.7 3056 10 26 32.8 1.7 465 10 27 32.8 1.7 269 10 28 32.8 1.7 269 10 31 32.4 1.7 1319 10 32 32.2 1.7 13029 10 34 32 1.7 13029 10 35 32 1.7 13029 10 36 32 1.7 13029 10 37 32 1.7 13029 10 38 31 1.8 1.6 1428 11 41 31 1.6 1428 11 42 31 1.6 1428 11 43 30.8 1.6 442 10
20 33.6 1.7 22 33.4 1.7 22 33.4 1.7 22 33.2 1.7 22 32.8 1.7 22 32.8 1.7 22 32.8 1.7 22 32.8 1.7 32.2 1
20 33.6 22 23.4 22 23.4 24 33.7 25 33.4 26 32.8 27 33.3 30 32.8 31 32.8 32 32.8 33 32.8 33 32.8 33 32.8 34 32.8 35 32.8 36 32.8 37 32.8 38 32.8 39 31.8 40 31.8 41.8 42 31.8 44 33.8 45 31.8 46 31.8 47 31.8 48 31.8 4
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## ALIGNMENTS

US-09-954-456-1583

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gequence 1883, Application US/09954456
Factor No. US2002011057A1
GENERAL INFORMATION:
Factor No. US2002011057A1
GENERAL INFORMATION:
FAPLICANTY Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
FILE REFERENCE: 689290-76
CURRENT FILING DATE: 2000-09-18
FRIOR FILING DATE: 2000-09-18
FRIOR FILING DATE: 2000-09-26
FRIOR FILING DATE: 2000-09-26
FRIOR FILING DATE: 2000-09-26
FRIOR PRILING DATE: 2000-09-25
FRIOR PRILING DATE: 2000-09-26
FRIOR FILING DATE: 2000-09-26
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FRIOR FILING DATE: 2000-09-27
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58.1%; Pred. No. 0.01;
iive 0; Mismatches 52;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1583
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Matches 72; Conservative
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                 417 CAACGTTGCGGACGTGGTGGTGGTGGCGCTTGGAGCGGTTTGGAGACGGCACGCAA 476
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                                                                                                                                                                                                                                                                   Sequence 2391. Application US/09880107
FPACENT NO. USZ0020142981A1
GENERAL INFORMATION:
APPLICANT: Wockley, Joseph G.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe.
CURRENT FILING DATE: 2001-06-14
FRIOR APPLICATION NUMBER: US 60/211,379
FRIOR FILING DATE: 2000-10-02
NUMBER OF SED ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M69177 US-09-880-107-2391
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58.1%; Pred. No. 0.01;
tive 0; Mismatches 52;
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APPLICANT: Elsaboff, Michael
APPLICANT: Blashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1612, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
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Matches 72; Conservative
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ORGANISM: Homo sapiens
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US-09-917-800A-1612
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LENGTH: 2491
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1679 AAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTCCAAG 1738
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US-09-917-800A-1612
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Patent No. US20020052308A1

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2000-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SEQ ID NO 562

LENGTH: 1386
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                       PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR PLILING DATE: 2001-06-06
PRIOR PLILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR PRILING DATE: 2001-06-19
PRIOR PRILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SSOFTWARE: PARCHAIN VET: 2.1
LENGTH: 2389
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NAME/KEY: misc_feature
LOCATION: (480)
OTHER INFORMATION: n equals a,t,g, or c
FILING DATE: 2000-07-31
APPLICATION NUMBER: US 60/222,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Rattus norvegicus
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ORGANISM: Homo sapiens
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Gaps 0;

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Length 314;

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427 GACGIGGIAGIGGIGGGCGCIGGCITGAGCGGITIGGAGACGGCACGCAAAGICCAGGCC 486
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APPLICANT: JWAMATION.

TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING

TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS

TITLE OF INVENTION: APAPTOSIS, AND ANTICANCER AGENTS

FILE REFERENCE: 4703/0F214

CURRENT APPLICATION NUMBER: US/09/912,176

CURRENT FILING DATE: 2001/07/24

PRIOR FILING DATE: 1999-01-22

PRIOR FILING DATE: 1999-01-22

PRIOR FILING DATE: 1998-05-22

PRIOR FILING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PATENTIN VET. 2.0
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Fatent No. US20020044941A1
GENERAL INPORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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                  ) ORGANISM: Bos taurus
; OTHER INFORMATION: CLone ID: 17-LIB34-060-Q1-E1-E9
US-09-960-352-3971
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Pred. No. 0.18;
                                                                                                     Score 37.2; DB 10;
Pred. No. 0.042;
0; Mismatches 53;
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Best Local Similarity 58.9%;
Matches 63; Conservative
                                                                                                       Query Match 1.9%;
Best Local Similarity 56.6%;
Matches 69; Conservative (
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US-09-925-302-242/c
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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF THE REFERENCE: 16511.006/37-21(10.294)
THE REFERENCE: 16511.006/37-21(10.294)
NUMBER OF SEQ ID NOS: 15112
LENGTH: 314
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                                       2.0%; Score 38; DB 10; Length 1386;
llarity 54.6%; Pred. No. 0.058;
Conservative 2; Mismatches 57; Indels
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Sequence 2009 Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, ID Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-06
PRIOR FILING DATE: 2001-05
NUMBER OF SEQ ID NOS: 8481
SEQ ID NO 239
SEQ ID NO 239
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61.0%; Pred. No. 0.068;
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                                    Query Match
Best Local Similarity
Matches 71; Conserv
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Matches 61; Conserv
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US-09-925-301-562
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1275 GGCGTCCGGCTGTATAGTACGATCGGCCTCGGGCGCGTGTTCCGAAGCAAAAAGGTGGT 1334
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                                                                                                                                                                                                                                                                                    Sequence 617, Application US/09925300 Patent No. US20020151681A1
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US-10-044-090-86
; Sequence 86, Application US/10044090
; Patent No. US20020137081A1
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Best Local Similarity 49.59
Matches 90; Conservative
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; ORGANISM: Homo sapiens
US-09-925-300-617
                                                                                                                                                       1395 GA 1396
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US-09-925-300-617
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APPLICANT: Horne, Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Wockley, Joseph G.
APPLICANT: Gone Logic, Inc.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 4491-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PALENTIN VET. 2.1
LENGTH: 1949
                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 35.2; DB 10; Length 3276; 52.8%; Pred. No. 0.81;
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Best Local Similarity 49.5%; Pred. No. 0.79;
Matches 90; Conservative 0; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                           NAME/KEY: misc feature
LOCATION: (125)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (455)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
                                                                                                                                                                                                                                                             LOCATION: (1014)
COTHER INFORMATION: n equals a,t,g, or c;
NAME/KEY: misc feature
LOCATION: (3276)
COTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-242
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                 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 242
LENGTH: 3276
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.89
Best Local Similarity 52.89
Matches 76; Conservative
 968
                                                                                          ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
NUMBER OF SEQ ID NOS:
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US-09-880-107-2388
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GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
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                                                                                         883 TAATGCGATCCTCCGACCTTGACTGCCAAGATTCACTTCAGACCAGAGCTTCCAGCAGA 942
823 AAGTGACAACATCATCATAGAGACGCTGAACCATGAACATTATGAGTGCAAATACGTAAT 882
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GENERAL INFORMATION.

APPLICANT: Craig Rosen,

APPLICANT: Craig Rosen,

TITLE OF INVENTION NUCLEIC Acids, Proteins and Antibodies

FILE REFERENCE: PA101

CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05988

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PALENTIN Ver. 2.0

SEQ ID NO 617
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ORGANISM: Homo sapiens
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Sequence 376, Application US/09925301

Patent No. US2020052308A1

GENERAL INFORMATION:

APPLICANT: ROSEON et al.

TILLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT APPLICATION NUMBER: DCT/US00/05882

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 376

LENGTH: 2018
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     ; NAME/KEY: misc_feature
; CTHER INFORMATION: Incyte ID No. US20020137081A1 1273213CB1
US-10-044-090-86
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                                                                                    Score 34.8; DB 12;
Pred. No. 1.2;
0; Mismatches 92;
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; Pred. No. 1.5;
0; Mismatches
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COTHER INFORMATION: n equals a,t,g, or c
NAME/KEI: misc_feature
LOCATION: (2012)
COTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-376
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1.8%;
Best Local Similarity 48.9%;
Matches 91; Conservative C
                                                                                      Query Match 1.8%;
Best Local Similarity 49.5%;
Matches 90; Conservative
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Sequence 339, Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REPERENCE: PA-0028 US
CURRENT APPLICATION UNMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 339
LENGTH: 3370
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                                          GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Cherk, Joseph G.
APPLICANT: Scherf, Uwe
TILE OF INVENTION: Gene Expression Profiles in Liver Cancer:
TILE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028-00.
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR PLING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1744
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Sequence 1744, Application US/09880107
Patent No. US20020142981A1
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illarity 48.9%;
Conservative (
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-044-090-339
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                                                                                                 236 AAATTTTTTTTTTTGTAGAGGATGTCTCGCCATGTTTCCCAAGCTGGTCTTGAACCCTGGCC 295
                                                                      379 GATGCCACGCCCTGGTGCCAGGACACTCGACCCCAGACGTTGCGGACGTGGTAGTG 438
                                                                                                                                                                439 GIGGGCGCTGGCTTGAGCGGTTTGGAGACGGCACGCAAAGTCCAGGCCGCCGGTCTGTCC 498
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                             0; Gaps
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1.8%; Score 33.8; DB 10; Length 401;
Best Local Similarity 48.6%; Pred. No. 0.62;
Matches 89; Conservative 1; Mismatches 93; Indels 0
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                          85; Indels
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Patent No. US20020045577A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefanson, Hreinn
APPLICANT: Stefanson, Hreinn
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
FRICA RAPLICATION NUMBER: US/09/795,668
PRIOR APPLICATION NUMBER: US/09/7156
PRIOR APPLICATION NUMBER: US/09/515,716
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1008
Best Local Similarity 50.0%; Pred. No. 2;
Matches 85; Conservative 0; Mismatches
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; ORGANISM: Homo sapiens
US-09-795-668-1008
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US-09-795-668-1008
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Title: Perfect score: Sequence:	US-09-771-045A-35 1929 1 atggcacttgcaccgagctagcctggtgccagcatag 1929
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FEATURES Location/Qualifiers  source 1.1929  Acrganism="unknown"  BASE COUNT 451 a 537 c 532 g 409 t  ORIGIN  Query Match 100.0%; Score 1929; DB 6; Length 1929;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 1929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	GGCCTCCCCAGCAGGTATTCC 60	Db   61 CACATCGGCGTAGGCCCAAACGAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120	Db 181 CTGCCAGCTTGCTGCAGTTGCAGCTCTTCAAACGACGTCACCAAGCTCAATTAC 240  Qy 241 TACATCGTCGACTACGCCCCGAGCAAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC 300  LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		421 GTTGCGGACGTGGTGGTGGCGCTGGCCTTGAGCGGTTTGGAGACGGCACGCAAAGTC 48	AAGACT 5 TGGATC 6	Oy         601 AATGACAGCAACGCAAGGGAAGTATCCAGATTGTATGAAGATTTGATTTGGAGGGCGAG 660           Db         601 AATGACAGCGAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGGCGAG 660           Collaborateraccaaccaaccaaccaactagaagtattacatttgaagattacattagaagaagaagaagaagaagaagaagaagaagaagaa	CCTTATGGTGACTCCCCGGTAAGCACAATCCCACTTTGTGATGAGACCTCTGTCGAGTGT 7  [	Db 841 GGAACTCCTCCCGGTAIGGTCTCAGCTGAAGAGTATAGCCTTGAAGACCCCAAGGC 900 Oy 901 GAGCCCTCAGGCGAAGCGGCTCGACGCTTCGCGCACTACTGTGAAGACCT 960 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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Location/Qualifiers
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Sequence 5 from patent US 6211435.
AR145474 1 GI:15107341
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Best Local Similarity 99.7%;
Matches 374; Conservative
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1 (bases 1 to 1392)
Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use patent: US 6211434-A 10 03-APR-2001;
Location/Qualifiers
Duvick, J.P., Gilliam, J.T., Maddox, J.R., Crasta, O.R. and Folkerts, O. Amino polyyol amine oxidase polynucleotides and related polypeptides and methods of use patent: US 6211435-A 5 03-APR-2001;
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Pred. No. 4.6e-168;
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AR145449
AR145449.1 GI:15107316
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1 (bases 1 to 1442)
Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.
Amino polyol amine oxidase polynucleotides and related polypeptides
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Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
Amino polyol amine oxidase polynucleotides and and methods of use
Patent: US 6211434-A 7 03-APR-2001;
Location/Qualifiers
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Pred. No. 4.6e-168;
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Sequence 7 from patent US 6211434.
AR145448 1 GI:15107315
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Location/Qualifiers
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Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
Amino polyol amine oxidase polynucleotides and amine mand methods of use
Patent: US 6211434-A 20 03-APR-2001;
                                                                                    Score 324; DB 6; 1
Pred. No. 4.6e-168;
0; Mismatches 1;
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and methods of use
Patent: US 6211435-A 7 03-APR-2001;
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1 (bases 1 to 1464)
Duvick, J.P., Gilliam, J.T., Maddox, J.R., Crasta, O.R. and Folkerts, O. Amino polyyol amine oxidase polynucleotides and related polypeptides and methods of under the control of an automatic US 6211435-A 20 03-APR-2001;
Location/Qualifiers
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Pred. No. 4.6e-168;
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Sequence 20 from patent US 6211435.
AR145483
AR145483.1 GI:15107350
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1 (bases 1 to 1803)
Duvick,J.P., Gilliam,J.T. and Maddox,J.R.

Duvick,J.P., Gilliam,J.T. and Maddox,J.R.

Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use

Patent: US 6211434.A 22 03-APR-2001;

Location,Qualifiers

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Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.
Amino polypol amine oxidase polynucleotides and related polypeptides and methods of use
Patent: US 6211435-A 16 03-APR-2001;
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1 (bases I to 1673)
Duvick, J. P., Gilliam, J.T. and Maddox, J.R.
Amino polyol amine oxidase polynucleotides
                                                                                                                                                                                                                                                                                                                                                                    Score 324; DB 6; I
Pred. No. 4.5e-168;
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Patent: US 6211434-A 16 03-APR-2001;
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Sequence 16 from patent US 6211435.
AR145481
AR145481.1 GI:15107348
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US 6211434.
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AR145454
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Best Local Similarity 99.7%;
Matches 374; Conservative 0
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                                                                                                                                                                                                                                                                                    Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 1803)

Buvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.
Amino polyyol amine oxidase polynucleotides and related polypeptides and methods of use
Patent: US 6211435-A 22 03-APR-2001;
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Pred. No. 4.5e-168;
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Sequence 22 from patent US 6211435.
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AR145484.1 GI:15107351
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Best Local Similarity 99.7
Matches 374; Conservative
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Unclassified.

1 (bases 1 to 1930)

Duvick,J.E., Gilliam,J.T. and Maddox,J.R.

Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use
Patent: US 6211434-A 39 03-APR-2001;
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       08-AUG-2001
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Pred. No. 4.5e-168;
0; Mismatches 1;
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1930 bp
Sequence 39 from patent US 6211434.
AR145466
AR145466.1 GI:15107333
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Best Local Similarity 99.7%;
Matches 374; Conservative
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Scoring table:

Word size :

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Minimum DB Maximum DB

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Perfect score:

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PCR primer N23259
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/*tag= a
/note="contains introns"
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21-MAY-1999;
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Exophiala spinifer
Amino polyol amine
DNA encoding an am
Amino polyol amine
DNA encoding an am
Amino polyol amine
DNA encoding an am
Amino polyol amine
DNA encoding amino
                                                                                                                           (without alignments)
10417.517 Million cell updates/sec
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| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001.ADT:*
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                                                                                                                                                                                                    1 atggcacttgcaccgagcta.....gcctggtgccagcagcatag 1929
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                                                                                                       November 12, 2002, 03:23:20 ; Search time 417 Seconds
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           5.1.3
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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           GenCore version
Copyright (c) 1993 - 2002
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                                                                        - nucleic search, using sw model
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AAZ58392
AAZ60630
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AAZ58393
AAZ60631
AAZ58393
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Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                                seq length: 0 seq length: 2000000000
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Result

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The present sequence is that of an isolated nucleic acid, designated ESP002_C2, of Exophiala spinifera isolate ESP002, which encodes an amino polyol amine oxidase (APAO, see AAY58900) capable of degrading fumonish, its hydrolysis product API, and related mycotoxins. The DNA was obtained by PCR amplification of related mycotoxins. The DNA was obtained by PCR amplification of ESP002 mycellal DNA using primers based on APAO of E. Spinifera ATCC 74269. The invention provides APAO polynucleotides (see AAX58383-87) and polypeptides (see AAY58900-05) of E. spinifera and AAX58383-87) and polypeptides (see AAY58900-05) of E. spinifera and plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Transgenic plants can be regenerated from the transformed plant cells. Also provided are methods for expressing both APAO and a fumonish-esterase in a transgenic plant, and for producing APAO enzyme in prokaryotic and non-plant eukaryotic systems. Transgenic plants capable of degrading fumonish or of perducing the degrading enzymes are provided. Methods for special containing the degrading enzymes are provided. Methods for expressing the degrading enzymes are provided. Methods for an animal feed and rumen microorganisms are also disclosed. APAO
                                                                                                                                                                                                                    New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed grain or in silage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1929 BP; 451 A; 537 C; 532 G; 409 T; 0 other;
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                                                                                                                                                                                                                                                                                                                       Claim 1; Page 137-138; 154pp; English
                                                                                           Maddox JR,
                  (PION-) PIONEER HI-BRED INT (CURA-) CURAGEN CORP.
                                                                                              JT,
                                                                                           Gilliam
                                                                                                                                          WPI; 2000-182425/16.
P-PSDB; AAY58900.
                                                                                              JP,
                                                                                              Duvick
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CACATCGGCGTAGGCCCAAACGAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120 Gaps 9 ATGGCACTTGCACCGAGCTACATCCCCCCAAACGTCGCCTCCCCCAGCAGGGTATTCC DB 21; Length 1929; ö Indels ; 100.0%; Score 1929; 100.0%; Pred. No. 0; Live 0; Mismatches Query Match 100. Best Local Similarity 100. Matches 1929; Conservative 61 61

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240 300 360 420 480 300 360 420 480 GACGCTTTGGGCGTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 180 CTGCGAGCTTGCCTTGCTGCAGCTGGAGCCTCTTCAAACGACGTCACCAAGCTCAATTAC CTGCGAGCTTGCCTTGCAGTTGGAGCCTCTTCAAACGACGTCACCAAGCTCAATTAC TACATCGTCGACTACGCCCCGAGCAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC GAATACCTCTTTGAGGTTGATGCCACGGCGCTGGTGCCAGGACACTCGACCCCCAGACAAC GTTGCGGACGTGGTAGTGGCGCGCTGGCTTGAGCGGTTTGGAGACGCCACGCAAAGTC TACATCGTCGACTACGCCCCGAGCAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC TTTGCCCTTGACAGGCTCCCTCCTTGCACGCTGGTGCCAGTACCGGCCTTGGCTTCACCT 181 241 121 121 181 241 301 361 361 421 421 301 g g g g ò g g 8 g ò ò ò ò ò ò

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The present sequence is that of an isolated nucleic acid, designated ESP002_C3, of Exophiala spinifera isolate ESP002, which encodes an amino polyol amine oxidase (APAO, see ARYS8901) capable of degrading fumonisin, its hydrolysis product API, and related mycotoxins. The DNA was obtained by PCR amplification of ESP002 mycolial DNA using primers based on APAO of E. spinifera ATCC 74269. The invention provides APAO polynucleotides (see AAXS833-87) and polypeptides (see AAYS8900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing plant cells normally susceptible to Fusarium or other toxin-producing changes infection. Transgenic plants can be regenerated from the transformed plant cells. Also provided are methods for expressing both APAO enzyme in prokaryotic and non-plant eukaryotic systems. Transgenic plants capable of degrading fumonisin or of producing the degrading enzymes are provided. Methods for cystems. Transgenic plants capable of degrading fumonisin or of producing the degrading enzymes are provided. Methods for detoxification of grain, grain processing, silage, food crops and channal feed and rumen microorganisms are also disclosed. APAO
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Pred. No. 0;
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 Claim 1; Page 139-140; 154pp; English.
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99.98;
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                                                               GCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCGCTCAGAACG
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The present sequence is that of polynucleotide k0n0-395_6.5, which encodes a truncated, but still functional, amino polyol amine oxidase canceds a truncated, but still functional, amino polyol amine oxidase (APAO, see AAYS9806). The polynucleotide was obtained by 3' and 5' RACE PCR using k0n0-395.5 (see AAZ58388), a partial APAO CDNA of Exophiala spinifera. APAO is capable of degrading fumonisin, its provides APAO polynucleotides (see AAZ58383-87) and polypeptides (see AAX58900-05) of E. Spinifera and Rhinocladialla atrovirens. The convention of Exophiale to Fusarium or other toxin-producing fungus infection. Also provided are methods for expressing APAO in transgenic plants, prokaryotic and non-plant eukaryotic systems. Methods for detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microcryanisms are also disclosed. APAO polynucleotide can also be used as a selectable marker.
                                                                                                                1741 GCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACG 1800
                                                                                                                                                                                                                                                                                                                                                                                                         transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed
                                                1801 CCGTTCAAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGGTATATG
                                                                                               GAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAAAGTTGTGGCTAGCCTGGTGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 324; DB 21; Length 1389; Pred. No. 1.8e-158;
                                                                                                                                                                                                                                                                                                                                                                                                     Amino polyol amine oxidase; fumonisin; mycotoxin; transgeni
detoxification; animal feed; silage; selectable marker; ss
                                                                                                                                                                                                                                                                                                                                                                       Amino polyol amine oxidase truncated DNA k0n0-395_6.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1389 BP; 332 A; 370 C; 395 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 74-76; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maddox JR;
                                                                                                                                                                                                                                                                          BP
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                                                                                                                                                                                                                                                                          CDNA; 1389
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-182425/16.
P-PSDB; AAY58906.
                                                                                                                                                                            1921 GCAGCATAG 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exophiala spinifera
                                                                                                                                                           GCAGCATAG 1929
                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           grain or in silage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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oxidase (APAO). The enzyme has homlology to the flavin containing amine oxidase family, that oxidise primary amine to an aldehyde or ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by ARAO generates, as a by-product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants own defensive systems. The APAO polynucleoxides are used to generate plants (particularly maize) that are resistant to Fusarium or other funging that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related sequences from other organisms. The APAO polypeptides are used to degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi, e.g. rumen microflora.
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                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                1015 CAATGETCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACGGTCC
                                                                                                                                                                                                                                                                                                                                                                                       1075 AAGCAGGTACGACAAAAAGTCTGTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1135 GCCCAAGTCCCAGAGCCGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1195 CAAGGAGCTCCGAGCGCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                  1675 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1735 CAAGGAGCICCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1795 AGAACGCCGTTCAAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                         Length 1389;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                          Sequence 1389 BP; 332 A; 370 C; 395 G; 292 T; 0 other;
                                                                                                                                                                                                                                                     Score 324; DB 21;
Pred. No. 1.8e-158;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amine oxidase DNA clone K:trAPAO.
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99.7%;
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                                                                                                                                                                                                                                                  Query Match 16.8
Best Local Similarity 99.7
Matches 374; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGCCAGCAGCATAG 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1375 GTGCCAGCAGCATAG 1389
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                                             1015 CAATGGTCCATTACCTGTTTCATGGTCGGAAGACCCGGGACGGAAGTGGTCCAACAGTGC 1074
                                                                                       1075 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1134
                                                                                                                                               GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAATCGAGTGGTCGAAGCAGCAGCAGTATTTC 1734
                                                                                                                                                              CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1794
                                                                                                                                                                                                                        1315 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial; plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
                              1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGCCCGGGACGGAAGTGGTCCCAACAGTCC 1614
                                                                                                                                                                                                                                                                AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAAÇGGAGACGTCTTTAGTTTGGAAAGGG 1854
                                                                                                                                                                                                                                                                                                                         TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG 1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes an Exophiala spinifera aminopolyol amine
      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding aminopolyol amine oxidase, used, generate plants resistant to Fusarium -
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding an aminopolyol amine oxidase clone trAPAO.
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/product= "aminopolyol amine oxidase"
    1;
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    Mismatches
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1..1389
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
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                                                                                                                                                                                                                                                                                                                                                                                   GTGCCAGCAGCATAG 1929
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   Conservative
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P-PSDB; AAY68843.
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374;
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   Matches
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The present sequence encodes an Exophiala spinifera aminopolyol amine oxidase (APAO). The enzyme has homlology to the flavin containing amine oxidase family, that oxidase primary amine to an aldehyde or ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by-product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants own defensive systems. The APAO polynucleotides are used to generate plants (particularly maize) that are resistant to Fusarium or other funging that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging); for recombinant production of APAO polypeptides, as selection markers for plant transformation; and to isolate related sequences from other organisms. The APAO polypeptides are used to degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi, e.g. rumen microflora.
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                                                                                                                             Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial; plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
                                                                                                                                                                                                                                                                                                                                                                                  /note= "the amino terminal Lys was added to the protein sequence for optimized expression"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1078 AAGCAGGTACGACAAAAGTCTGTGTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding aminopolyol amine oxidase, used, e.g. generate plants resistant to Fusarium -
                                                                           DNA encoding an aminopolyol amine oxidase clone K:trAPAO.
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                                                                                                                                                                                                                                                                                                                                                          /product= "aminopolyol amine oxidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 324; DB 21;
Pred. No. 1.8e-158;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gilliam JT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC (CURA-) CURAGEN CORP.
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99.7%;
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                            (first entry)
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/*tag=
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                                                                                                                                                                                                                             Exophiala spinifera.
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Matches 374; Conserv
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                          16-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JAN-2000
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                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                                                                                 Key
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                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of a polynucleotide encoded a truncated, but still functional, amino polyol amine oxidase (K:trAPAO, see AAY5899) of Exophiala spinifera. The polynucleotide was derived from clone k0n0-395_6.5 (see AAZ5832) to which was added a 5' lysine codon (nucleotides 1-3), since many amine oxidases have a positively charged amino acid near the N-terminus and upstream of a dinucleotide binding capte. The construct allowed heterologous expression of trAPAO in plotha pastoris and maize. The polynucleotides APA58983-87) and polypeptides (see AAY58900-05) of E. spinifera and Rainocladdella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Also provided are methods for expressing APAO in transfernic captoxification of grain, grain processing APAO in transfernic detoxification of grain, grain processing sites, food crops and in animal feed and rumen microorganisms are also disclosed. APAO polynucleotide can also be used as a selectable marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCCAACAGTCC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1318 TATATGGAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGGCTAGCCTG 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1018 CAATGGTCCATTACCTGTTTCATGGTCGGAGAACCCGGGACGGAAGTGGTCCCAACAGTCC 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1078 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1137
                                                                                                                                                                                                                                                       New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1138 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTGGTGGAGCAGCAGTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATATGGAAGGGCCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAACGCCGTTCAAGTGTGTTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.8%; Score 324; DB 21; Length 1392; llarity 99.7%; Pred. No. 1.8e-158; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1392 BP; 335 A; 370 C; 395 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                          Example 7; Page 81-83; 154pp; English.
                                                                                                                             Maddox JR;
                                              (PION-) PIONEER HI-BRED INT INC. (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ60633 standard; DNA; 1392 BP.
  99US-0135391
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                                                                                                                          Duvick JP, Gilliam JT,
                                                                                                                                                                         WPI; 2000-182425/16.
P-PSDB; AAY58909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 374; Conserv
                                                                                                                                                                                                                                                                                                           grain or in silage
21-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ60633;
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Maddox JR;

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Indels

Length 1392;

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1915

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AAZ60633 ID AAZ6 RESULT 6

1734

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Location/Qualifiers
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                                                                               Query Match
Best Local Similarity 99.7%;
Matches 374; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number= 1
647..699
/*tag= c
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/*tag= d
/number= 2
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                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                         1915 GTGCCAGCAGCATAG 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /number=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of polynucleotide k0n0-395_5.4, which encodes a truncated, but still functional, amino polyol amine oxidase (trAPAO-1, see AAY58907 and AAY58908). The polynucleotide was obtained by 3' and 5' RACE PCR using k0n0-385.5 (see AAZ58888), a partial APAO CDNA of Exophiala spinifera. APAO is capable of degrading fumonisin, its hydrolysis product AP1 and related myxotoxins. The invention provides APAO polynucleotides (see AAZ58383-87) and polypeptides (see AAZ58900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Also provided are methods for expressing APAO in transgenic plants,
             1198 CAAGGAGCTCCGAGCGCTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1257
                                                         1914
                                                                                                       CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed
                                                                                                                                                                                                                                                                                                              Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ss.
                                                                                         1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG
                                             1795 AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
                                                                                                                                                                                                                                                                                        Amino polyol amine oxidase truncated DNA k0n0-395_5.4.
                                                                                                                                                                                                                                                                                                                                                                                 1..1442
/*tag= a
/note= "contains an intron"
647.699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Page 77-79; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maddox JR;
                                                                                                                                                                                                                     AAZ58393 standard; cDNA; 1442 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PION-) PIONEER HI-BRED INT INC (CURA-) CURAGEN CORP.
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99US-0135391.
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P-PSDB; AAX58907, AAX58908.
                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                    1378 GTGCCAGCAGCATAG 1392
                                                                                                                                       GTGCCAGCAGCATAG 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gilliam JT,
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                                                                                                                                                                                                                                                                                                                                               Exophiala spinifera.
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                                                                                                                                                                                                                                                                 23-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                    intron
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AAZ58393
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                                                                                                                                                                                                                                                                                                                                                                                   1068 CAATGGTCCATTACCTGTTTCATGGTCGGAAGACCCGGGAAGGTGGTCCCAACAGTCC 1127
                                                                                                                                                                                                                                                                                                                                                     Gaps
prokaryotic and non-plant eukaryotic systems. Methods for detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed. APAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1128 AAGCAGGTACGACAAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1188 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGCAGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1308 AGAACGCCGTTCAAGAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1675 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1735 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACATTGGGGTTCGGCGTC
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                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                            Length 1442;
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                                                                                                                                                                                                                                                                                       Indels
                                                                                               polynucleotide can also be used as a selectable marker
                                                                                                                                                             Sequence 1442 BP; 336 A; 381 C; 416 G; 309 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "aminopolyol amine oxidase"
                                                                                                                                                                                                                        Score 324; DB 21;
Pred. No. 1.8e-158;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "contains an intron"
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(first entry)

Location/Qualifiers

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DNA encoding amino polyol amine oxidase for expression in
                                                                                   Amino polyol amine oxidase; APAO; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; barley; alpha-amylase; signal peptide;

    Exophiala spinifera.

                                                                                                                                                        Chimeric - Hordeum vulgare
                               23-MAY-2000
                                                                                                                                                                                                               sig_peptide
    AAZ58401;
                                                                                                                                                                      Chimeric
  ö
                                                                                                                                                                                                                                             The present sequence encodes an Exophiala spinifera aminopolyol amine oxidase (APAO). The enzyme has homlology to the flavin containing amine oxidase family, that oxidise primary amine to an aldehyde or ketone,
                                                                                                                                                                                                                                                                                    releasing ammonia and hydrogen percoxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants own defensive systems. The APAO polynucleotides are used to generate plants for that are resistant to Fusarium or other fungitate that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related sequences from other organisms. The APAO polypeptides are used to degrade mycotoxins in plant materials, including expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1555 CAATGGTCCATTACCTGTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1068 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1675 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAATCGAGTGGTCGAAGCAGCAGTATTTC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG 1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1188 GCCCAAGTCCCAGAGCCGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGGAGCICCGAGCGCCGICTAIGGGCIGAACGAICTCATCACACIGGGITCGGCGCIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1308 AGAACGCCGTTCAAGAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTTGGAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG
                                                                                                                                                                                  e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1442;
                                                                                                              Maddox JR;
                                                                                                                                                                               New nucleic acid encoding aminopolyol amine oxidase, used, generaté plants resistant to Fusarium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1442 BP; 336 A; 381 C; 416 G; 309 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           engineered bacteria and fungi, e.g. rumen microflora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 324; DB 21;
Pred. No. 1.8e-158;
0; Mismatches 1;
                                                                                                             Gilliam JT,
                                                                                                                                                                                                                       Example 6; Page 78-80; 145pp; English.
                                                                                                             Folkerts O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.8%;
99.7%;
                                        98US-0092936
                                                                  (PION-) PIONEER HI-BRED INT (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 374; Conservative
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                                                                                                             Duvick J,
                                                                                                                                       WPI; 2000-182426/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                    P-PSDB; AAY68844
            08-JUL-1999;
                                        15-JUL-1998;
                                                                                                             Crasta OR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "barley alpha-amylase signal peptide"
73..1461
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          crops and in animal feed and rumen microorganisms are also on the solynucleotide can also be used as a selectable marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1464 BP; 343 A; 405 C; 409 G; 307 T; 0 other;
                                                                                                                                                                                                                                    /note= "extra lysine codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 11; Page 94-96; 154pp; English.
                                                                                                                                   /product= "K:trAPAO"
73..75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maddox JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PION-) PIONEER HI-BRED INT (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US15454
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/*tag= a
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P-PSDB; AAY58912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      grain or in silage
                                                                                                                                                                                                                                                                                                        WO200004159-A1
                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998
                                                                       mat_peptide
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AAZ58401 standard; cDNA; 1464 BP.

RESULT 9

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Matches 374;
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                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                              Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial; plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
                                                                                                                                  1389
                                           1675 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC 1734
                                                   1090 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCGGGACGGAAGTGGTCCCAACAGTCC 1149
                                                                        1735 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGTC
                                                                                                      AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
                                                                                                              DNA encoding an aminopolyol amine oxidase for expression in malze.
               1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGG
                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
/note= "aminopolyol amine oxidase, with an extra
amino terminal Lys residue for optimized
                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/note= "barley alpha amylase signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maddox JR;
                                                                                                                                                                                                                                                                                                                                                        /product= "aminopolyol amine oxidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gilliam JT,
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    expression"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Folkerts O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC. (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                     AAZ60640 standard; DNA; 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US15455.
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/*tag= c
                                                                                                                                                                 GTGCCAGCAGCATAG 1929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-182426/16.
P-PSDB; AAY68848.
                                                                                                                                                                                                                                                                                                                    Exophiala spinifera.
                                                                                                                                                                                                                                                                                                      Hordeum vulgare.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200004160-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JAN-2000.
                                                                                                                                                                                                                                                   16-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                    AAZ60640;
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                                                                                                                                                                  1915
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The present sequence encodes an Exophiala spinifera aminopolyol amine oxidase (APAO). The APAO enzyme has homlology to the flavin containing amine oxidase family, that oxidase primary amine to an oxidase family, that oxidase primary amine to an addehyde or ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants own defensive systems. The APAO polynucleotides are used to generate plants (particularly maize) that are resistant to Fusarium or other fungict that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related sequences from other organisms. The APAO polypeptides are used to degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi, e.g. rumen microflora.
                                                                                                                                                                                                                                                                                                                                                                                                                    fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1330 AGAACGCCGTTCAAGAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG 1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1150 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGGGGCAGCCTACGAGAACGCCGGG 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAACGCCGTTCAAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG 1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGGAGCICCGAGCGCCGICIAIGGGCTGAACGAICTCAICACACIGGGTICGGCGCIC 1794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGCCCGGGACGGAAGTGGTCCCAACAGTCC 1614
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e.g.
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0
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Pred. No. 1.8e-158;
0; Mismatches 1; Indels 0;
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New nucleic acid encoding aminopolyol amine oxidase, used, generate plants resistant to Fusarium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino polyol amine oxidase; APAO; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; alpha mating factor; signal peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1464 BP; 343 A; 405 C; 409 G; 307 T; 0 other;
                                                                                                   Example 11; Page 95-97; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Saccharomyces cerevisiae.
Chimeric - Exophiala spinifera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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ilarity 99.7%;
Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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2000-182426/16.
                                                                                                                                                                                                                                                                                                                                        Synthetic.
Exophiala spinifera.
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                                                                                                                                                                                                                                                          16-MAY-2000
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                                                                                                                                                                                                                                                                                                        Aminopolyo1
                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
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                                                                                                                                                                                                                                     AAZ60638;
                                                                                                                                                                                                                                                                                                                    plant
                  1471
                                         1795
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                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of polynucleotide ppiczalphaA:K:trAPAO cencoding a protein (see AAY58910) comprising the yeast alpha mating factor signal peptide fused with K:trAPAO, a truncated, but functional, amino polyol amine oxidase (APAO, see also AAY58909) of functional, amino polyol amine oxidase (APAO, see also AAY5809) of functional aspinifera. The polynucleotide was designed for expression in Pichia pastoris. The encoded protein is capable of degrading fumonisin and related mycotoxins. The invention provides APAO of polynucleotides (see AAY58083-87) and polypeptides (see AAY58000-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Rusarium or other toxin-producing fingus infection. Also provided are methods for expressing, silage, food crops and in animal feed and rumen microorganisms are also disclosed. APAO polynucleotide can also be used as a selectable marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1351 AAGCAGGTACGACAAAAAGTCTGTCTGGGACCAACTCCGCGCGGCGTACGAGAACGCCGGG 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1291 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCCAGCCTACGAGAACGCCGGG 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1675 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1411 GCCCAAGTCCCGAGGCGGCCAACGTGCTCGAAATCGAGTGGAGGCAGCAGCAGTATTC 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1735 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed grain or in silage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                              "yeast alpha mating factor secretion signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1673 BP; 414 A; 430 C; 456 G; 373 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 324; DB 21;
Pred. No. 1.8e-158;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                          Example 8; Page 85-87; 154pp; English.
                                                                                                                                /*tag= d
/note= "extra lysine"
Location/Qualifiers
1..1665
                                                                                                           "K:trAPAO'
                                                                                                                                                                                                                                                                                                       Maddox JR;
                                                                                                                                                                                                                                                                     PION-) PIONEER HI-BRED INT INC.
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0
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/product= '
268..270
                                                               /product=
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                                                                                     268..1662
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                           /*tag=
1..267
/*tag=
                                                                                                                                                                                                                                                                                                      Gilliam JT,
                                                                                                                                                                                                                                                                                CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                 WO200004159-A1
                                                                                                                     misc_feature
                                                                                                                                                                                                             08-JUL-1999;
                                                                                                                                                                                                                                  15-JUL-1998;
21-MAY-1999;
                                                                                                                                                                                       27-JAN-2000
                                         sig_peptide
                                                                                     mat_peptide
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The present sequence encodes a Exophiala spinifera aminopolyol amine oxidase (APAO). The enzyme has homlology to the flavin containing amine oxidase family, that oxidise primary amine to an aldehyde or Ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by-product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants own defensive systems. The APAO polynucleotides are used to generate plants (particularly maize) that are resistant to Fusarium or other fungi
                                                                                                                                                               oolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial; fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..267
/*tag* b
//otote* "yeast alpha mating factor secretion signal"
268..1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding an aminopolyol amine oxidase for expression in Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                  AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
                                                                                                                                TATATGGAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding aminopolyol amine oxidase, used, e.g. generate plants resistant to Fusarium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gilliam JT, Maddox JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "aminopolyol amine oxidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "aminopolyol amine oxidase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ60638 standard; DNA; 1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US15455,
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                                                                                                                                                                                                                                                                                                    GIGCCAGCAGCAIAG 1665
                                                                                                                                                                                                                                                          1915 GTGCCAGCATAG 1929
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Exophiala spinifera.
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Matches 374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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AAZ60641
ID AAZ60
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that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related sequences from other organisms. The APAO polypeptides are used to degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi, e.g. rumen microflora.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1591 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGGTTAGCCTG 1650
                                                                                                                                                                                                                                                                                   1855 TATATGGAAGGGCCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCCTAGCCTG 1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1794
                                                                                                                                                                                                                                                             CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
                                                                                                                                                                                                                                                                                                                                           1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGACGCCGGG 1674
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ds.
                                                                                                                                                                                                                                                                                                                                                                 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1795 AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGCGTCTTTAGTTTGGAAAGGG
                                                                                                                                                                                                                        ;
0
                                                                                                                                                                               Length 1673;
                                                                                                                                                                                                                        Indels
                                                                                                                                          Sequence 1673 BP; 414 A; 430 C; 456 G; 373 T; 0 other;
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                                                                                                                                                                               Score 324; DB 21;
Pred. No. 1.8e-158;
                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ58402 standard; cDNA; 1803
                                                                                                                                                                             16.8%;
ilarity 99.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gilliam JT,
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P-PSDB; AAY58913.
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                                                                                                                                                                                                 Similarity
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21-MAY-1999;
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                                                                                                                                                                                                     Best Local Simmatches 374;
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                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                              of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
New isolated polynucleotides, polypeptides useful for detecting and degrading fumonish or structurally related mycotoxin in processed grain or in silage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1429 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACACTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1803 BP; 424 A; 501 C; 502 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 324; DB 21;
Pred. No. 1.8e-158;
0; Mismatches 1;
                                                                                                                                          Example 10; Page 97-100; 154pp; English.
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99.7%;
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1915 GTGCCAGCAGCATAG 1929
                                                             RESULT 15
AAZ58384
ID AAZ58;
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                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a full length Exophiala spinifera aminopolyol amino oxidase (APAO). The enzyme has homlology to the aminopolyol amine oxidase family, that oxidise primary amine to an aldehyde or ketone, releasing ammonia and hydrogen peroxide.

The APAO enzyme degradese mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by-product, plants own defensive systems. The APAO polynucleotides are used to generate plants (particularly maize) that are resistant to fusarium or coher fungi that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging): for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to clayeptides; as selection markers for plant transformation; and to clayeptides as selection markers for plant transformation; and to care used to degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi, e.g. rumen microflora.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1669 AGAACGCCGTTCAAGAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG 1728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                     New nucleic acid encoding aminopolyol amine oxidase, used, e.g. to generate plants resistant to Fusarium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1735 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC
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16.8%; Score 324; DB 21; Length 1803; Best Local Similarity 99.7%; Pred. No. 1.8e-158; Matches 374; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                          Maddox JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1803 BP; 424 A; 501 C; 502 G; 376 T; 0 other;
                                                 /product= "aminopolyol amine oxidase"
                                                                                                                                                                                                                         Gilliam JT,
                                                                                                                                                                                                                                                                                                                                 Example 10; Page 99-101; 145pp; English.
           Location/Qualifiers
1..1803
/*tag= a
                                                                                                                                                                                                                          Folkerts O,
                                                                                                                                                                                (PION-) PIONEER HI-BRED INT INC (CURA-) CURAGEN CORP.
                                                                                                                                                         98US-0092936.
                                                                                                                                99WO-US15455.
                                                                                                                                                                                                                         Crasta OR, Duvick J,
                                                                                                                                                                                                                                                  WPI; 2000-182426/16.
                                                                                                                                                                                                                                                                P-PSDB; AAY68849
                                                                             WO200004160-A1
                                                                                                                              08-JUL-1999;
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The present sequence is that of an isolated nucleic acid, designated ESP003_C12, of Exophiala spinifera isolate ESP002, which encodes an amino polyol amine oxidase (APAO, see AAY58902) capable of degrading fumonishi, its hydrolysis product API, and related mycotoxins. The DNA was obtained by PCR amplification of ESP003 mycelial DNA using primers based on APAO of E. spinifera ATCC 74269. The invention provides APAO polynucleotides (see AASS883-87) and polypeptides (see AAYS8900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to ransform plant cells normally susceptible to Fusarium or other toxin-producing plant cells infection. Transpenic plants can be regenerated from the transformed plant cells. Based provided are methods for expressing both APAO and a fumonisin-esterase in a transgenic plant, and for systems. Transgenic plants capable of degrading fumonisin or of producing the degrading enzymes are provided. Methods for detoxification of grain, grain processing, sliage, food crops and in animal feed and rumen microcapanisms are also disclosed. APAO APAO APAO Colynucleotide is also useful as a selectable marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed grain or in silage \varepsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ds.
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/note= "contains introns"
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1..1930
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1134..1187
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1789 GTGCCAGCAGCATAG 1803
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21-MAY-1999;
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                                                                                                                                                                                                        1736 CAAGGAGCCCGAGCGCCTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1795
                                                                                                            1616 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAAAGCCCGG 1675
                                                                                              1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674
                                                                                                                                             1675 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC 1734
                        Gaps
                        0;
Ouery Match 16.8%; Score 324; DB 21; Length 1930; Best Local Similarity 99.7%; Pred. No. 1.8e-158; Matches 374; Conservative 0; Mismatches 1; Indels 0
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Search completed: November 12, 2002, 05:41:50 Job time : 425  $\sec s$ 

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November 12, 2002, 04:43:45; Search time 2811 Seconds (without alignments) 11113.872 Million cell updates/sec
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1929
1 atggcacttgcaccgagcta.....gcctggtgccagcagcatag 1929
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                        16154066 seqs, 8097743376 residues
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                                                                                 OM nucleic - nucleic search, using sw model
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	8: em_gss_
	6: em_gss_
	0: em_
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	5: em_
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	27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
		46				
Result No.	Score		Query Match Length DB ID	DB	ID	Description
1	23	1.2	623	17	1.2 623 17 AQ280543	AQ280543 CITBI-E1-
0	21	1.7	1284	14	BM803905	BM803905 AGENCOURT
3	20	1.0	285	13	BI050480	BI050480 CM3-GN031
O 4	20	1.0	434	17	AQ046343	AQ046343 RPCI11-34
S	20	1.0	526	17	17 AQ697937	AQ697937 HS_5536_B
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2 2-42 9 Pan 3 SALK 5 P2T1 DKFZP 7 6013	4866 6011 44854 1L5- 3091 6016 44571 6016 44855 1L5- 6968 6024		1027 1000 1000 1000 1000 1000 1000 1000
72 4 4 4 4 4 4 4 5 5 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	BE264266 BE796178 BE714854 BE903091 BF204571 BE714855 BG3868	BG386332 BG386332 BE200064 BE207669 BE27625 BE207625 BE306488 BF306482 BF306482 BF306482 BE306412 BM875102 BG152936	
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## ALIGNMENTS

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DNA sequence.
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AQO46343.1 GI
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/db_xref="taxon:9606"
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/note="Site_2" Sall; Cloned unidirectionally. Primer: Oligo dT.
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                 /sex="male"
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/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
calTech Human BAC Library D"
a 192 c 94 g 200 t 1 others
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1 (bases 1 to 1284)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.lln.gov
Plate: LLAM12184 row: o column: 06
High quality sequence stop: 453.
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                                                                                                                                                                                                                                                                         Query Match 1.2%; Score 23; DB 17; Length 623; Best Local Similarity 100.0%; Pred. No. 0.81; Matches 23; Conservative 0; Mismatches 0; Indels
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Mismatches
                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="251406"
/clone_lib="CITBI-E1"
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Tissue Procurement: ATCC
                                                       Location/Qualifiers
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// organism="Homo saplens"

/db_xref="taxon:9606"
/clone_lib="cN0313"
/dev_stage="Adult"
/note="Organ: placenta_normal; Vector: puc18; Site_1: Sma!
/ site_2: Sma!, A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
                                                                                                                                                                                            Homo sapiens
Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 285)
10 Jas Neto.2., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scriptss/gethtml2.plrtl-CM3&t2=CM3-GN0313-050101-593-e06&t3=200101-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 285.
Location/Qualifiers
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RPCIII-34I18.TK RPCI-11 Homo sapiens genomic clone RPCI-11-34I18,
BIO50480 285 bp mRNA linear EST 15-JUN-2001 CM3-GN0313-050101-593-e06 GN0313 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Matches 20, Conservative
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/note="Wector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector sites ites. 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU133639 716 bp mRNA linear EST 01-AUG-2002 AU133639 OVARC1 Homo sapiens cDNA clone OVARC1000332 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 716)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
               library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 112 row: N column: 17
Seg primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genomics@hri.co.jp Helix wan con a project, 5. \epsilon 3'-end one pass sequencing: Helix Hern human cDNA project, 5. \epsilon 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and
Clones are derived from the human BAC library RPCI-11. For BAC
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                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=1112 Col=17 Row=N"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0%; Score 20; DB 17; Length 526; 100.0%; Pred. No. 35; 7ative 0; Mismatches 0; Indels
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
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//tissue_type="Covary, tumor tissue"
/note="Vector: pME18SFL3"
197 c 193 g 155 t 3
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/db_xref="taxon:9606"
/clone="OVARC1000332"
                                                                                                                                                                                                                       High quality sequence stop: 526.
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Genomics Laboratory
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                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Butheria; Primates; Catarrhini, Hominidae; Homo.

E I (bases 1 to 434)

E Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Mible, C., de Jong, P. and Venter, J.C.

Use of BAC End Sequences for Sequence-Ready Map Building (1998)

L Unpublished (1998)

Londert: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Madical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200

Fax: 301 838 0200
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AQ697937.1 GI:5388185
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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                                                                                                                                                                                                                                                                                                                                                             Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library ovallability, please contact Pleter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@ressgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
Location/Qualifiers
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCILL Human Male BAC Library"
80 9 145 t
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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University of Washington
University of Washington
Voll Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:7512881"
/db_xref="taxon:9606"
/clone="RPCI-11-34118"
/clone_lib="RPCI-11"
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100.0%; Pre
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                                                                                                   AUTHORS
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                                             AG059979 922 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-047F09.R, genomic survey sequence.
AG059979
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fuliyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
271 c 355 g 243 t 2 others
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/db_xref="taxon:9598"
/clone="PTB-047F09.R"
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R.Site 2 : SacI.
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   RESULT 8
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BH811443
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/cultivar="Landrace"
/db xrof="laston:55670"
/clone_lib="stevia field grown leaf cDNA"
/tissue_type="leaf"
/tissue_tisue_tool grown ind.size_tisue
/tissue_tisue_tool
/tissue_tisue
                                                                                                                                                                                                                                                                                                                                                                                         BG522272 807 bp mRNA linear EST 01-FEB-2002 2-42 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
Contact: Jim Brandle
Contact: Jim Brandle
Genomics and Biotechnology
Agriculture and Agri-Food Canada - SCPFRC
1391 Sandford St., London, Ontario, CANADA, NSV 4T3
T=1: 519 457 1470
Fax: 519 457 3997
Email: brandleje@em.agr.ca
Score 20; DB 9; Length 716;
Pred. No. 37;
0; Mismatches 0; Indels
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/organism="Stevia rebaudiana"
/strain="751/1501"
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Pred. No. 38;
0; Mismatches
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Location/Qualifiers
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100.0%; Pre
   Query Match 1.0%; Sc
Best Local Similarity 100.0%; P.
Matches 20; Conservative 0;
                                                                                                                                           1667 ACGCCGGGCCCAAGTCCCA 1686
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Matches 20, Conservative
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SALK_058617 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_058617, DNA sequence.
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homoso, "M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
                                                                                                                                                                                                                                                                             Arabidopsis thaliana
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 80)
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Gaps

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181 bp mRNA linear EST 22-MAR-2002
DKFZp686H1969_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686H1969 5', mRNA sequence.
/clone_lib="Plasmodium yoelii infected liver tissues"
/tissue_type="liver"
/note="Organ: liver; P. yoelii sporozoites were IV
injected into BALB/c mice and livers were harvested 24
hours post injection. Total RNA was processed and
differential display was performed on the infected liver
samples along with uninfected BALB/c liver control."

16 c 19 g 53 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (Buropean Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S. EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S. Unpublished (1999)
Contact: Ansorge W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="DHIOB"
/note="Vector: prriplEx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
57 c 64 g 31 t 3 others
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6, 14059
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This clone (DRFZp688H1965) is available at the RZPD in
Please contact the RZPD: Ressourcenzentrum, Heubnerweg
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                            Length 119;
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/db_xref="taxon:9606"
/clone="bkFzpe86Hip969"
/clone_lib="686 (synonym: hlcc3)"
/tissue_lype="human skeletal muscle"
                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                         DB 10;
89;
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Pred. No. 98;
0; Mismatches
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100.0%; Pred. No.
tive 0; Mismatch
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100.0%; Piv
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                                                                                                                                                                                                                                                                                                                                                                                              /db.zare="crammora"
/db.zare="crammora"
/db.zare="salkx 058617"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/clone="salkx 058617"
/clone=lib="Arabidopsis thaliana Inses"
/note="pcR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
22 c 15 g
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                                                                                                                                                                                                                     This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At1947210 and an annotated exon of At1947210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 119)
Lau, A.O. T., Sacci, J.B. Jr and Azad, A.F.
Retrieving parasite specific liver stage gene products in Plasmodium yoelii infected livers using differential display Mol. Blochem. Parasitol. 111, 143-151 (2000)
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Dept. of Microbiology and Immunology
Diversity of Maryland, Baltimore
655 W. Baltimore Street, BRB 3-034, Baltimore, MD 21201, USA
Tel: 410-706-7066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
       Sequence-Indexed Library of Insertion Mutations in the
                     Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 19; DB 17; Length 80; 100.0%; Pred. No. 82;
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                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
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Insert Length: 119 Std Error: 0.00.
Location/Qualifiers
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                  /strain="Columbia 0"
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: IGTTATAACTGTATTTAC
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100.0%; Pic
0; }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: alau@umaryland.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW783945
AW783945.1 GI:7838321
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 GCCTTGGCTTCACCTGAAT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GCCTTGGCTTCACCTGAAT 79
                                                                                                                                                                                                                                                                     an annotated exon c
Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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les 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
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AW783945
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TITLE
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                                                JOURNAL
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       TITLE
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g δλ

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/organism="Triticum aestivum"
/cultivar="Butte 86"
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/tissue_type="whole grains"
/tissue_type="whole grains"
/tissue_type="whole grains"
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/dev_stage="3.4 days post anthesis seed"
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/note="yector: Lambda ZAP II, excised phagemid; Site_I:
ECORI; Plants were grown under six following different
environmental regimes in greenhouse, Environment I)
240c/170c day/nipht, well-watered, without post-anthesis
fertilizer, Environment 2) 240c/170c day/night,
/well-watered, without post-anthesis fertilizer,
Environment 3) 370c/170c day/night plus drought, with
post-anthesis fertilizer, Environment 4) 370c/170c
day/night plus drought, without post-anthesis fertilizer,
Environment 5) 370c/170c day/night plus drought, without post-anthesis fertilizer,
day/night plus drought, without post-anthesis fertilizer,
environment 5) 370c/170c
day/night plus drought, without post-anthesis fertilizer,
Day/night plus drought, without post-anthesis fertilizer,
day/night plus drought, without post-anthesis fertilizer,
environment 5) 370c/170c
day/night plus drought, without post-anthesis fertilizer,
Day/night plus drought, without post-anthesis fertilizer,
day/night plus drought, without post-anthesis fertilizer,
Day 32, 34, 10, 12, 16, 20, 24, 28, 35, 7, 8, 10, 12, 16, 20, 24, 28, 30, 32, 34, DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S.

20, 24, 28, 30 DPA and total RNA was prepared by S.

21, 22, 33, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S.

22, 24, 28, 30 DPA and total RNA was prepared by S.

23, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S.

22, 24, 28, 30 DPA and total RNA was prepared by S.

23, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
11: 5105595773
Fax: 5105595818
Email: candersnepw.usda.gov
Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE264866 185 bp mRNA linear EST 13-JUL-2000 601194354F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538309 5',
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE264866.1 GI:9138427
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BE264866
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Best Local Similarity
Matches 19; Conserv
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BE264866/c
LOCUS
DEFINITION
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      COMMENT
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                                                                                                                                                                                                                               Bukaryofa, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 182)

S NIH-MGC http://mgc.ncl.nih.gov/.

S NIH-MGC http://mgc.ncl.nih.gov/.

I (npublished (1999)

C Contact; Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

C Naturary Preparation: Ling Hong/Rubin Laboratory

C DNA Library Preparation: Ling Hong/Rubin Laboratory

C DNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MESSY3_E02_J03zS Wheat developing grains cDNA library Triticum aestivum cDNA clone WHE3573_E02_J03, mRNA sequence.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticaea; Triticum.
1 (bases 1 to 184)
Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin
Altenbach, S., Anderson, C.D., Lazo, G.R., Pham, J., Rausch, C.J.,
Wilson, C. and Woo, J.
The structure and function of the expressed portion of the wheat
genomes - Developing grains CDNA library
Unpublished (2002)
   BE560457 116-2000 mRNA linear EST 15-AUG-2000 601346723F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687725 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage resistant)"
/note="Organ: lymph; vector: poTB); Site_1: XhoI; Site_2:
ECORI; CDNA made by Oligo-dr priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCAGGAGG, Size-selected >500bp for average
insert size I.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies):"
5 c 60 g 31 t
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Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence start: 3
High quality sequence stop: 182.
Location/Qualifiers
1. 182
/organism="Nomo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3687725"
/clone="IMAGE:3687725"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.00,0%; Pre-
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                                                                                                                       BE560457.1 GI:9804177
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Best Local Similarity 100.
Matches 19; Conservative
                                                          mRNA sequence.
BE560457
                                                                                                                                                                                                               Homo sapiens
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                                                                                       ACCESSION
VERSION
KEYWORDS
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AUTHORS
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AUTHORS
TITLE
JOURNAL
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BQ805991
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KEYWORDS
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ò q

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone='Insage:3538309"
/clone='Insage:3538309"
/clone=lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH108 (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: Goorl: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE796178 20-SEP-2000 601591321F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945316 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: lung; Vector: POTB7; Site_1: XhoI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM803 row: column: 05

High quality sequence stop: 201.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Plate: LLCM223 row: k column: 14
High quality sequence start: 4
High quality sequence start: 4
High quality sequence stop: 185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
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/db_xref="taxon:9606"
/clone="IMAGE:3945316"
                                                                                                                                                                                   Location/Qualifiers
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BE796178
BE796178.1 GI:10217376
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ECORI; CDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected 5500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                 Score 19; DB 12; Length 201;
Pred. No. 1e+02;
0; Mismatches 0; Indels
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AQ280543 622-NOV-1998 CITBI-E1 Homo sapiens genomic clone 251406, DNA sequence.
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Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Buteleostomi;

Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.

1 (bases 1 to 623)

Adams, M.D... Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,

Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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BM873502
BM752936
BG152936
A7414414
BE380159
BE380159
AA719264
BH317104
AA013604
AA013604
BM829459
AA542887
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BM755698
AI450161
AW504032
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BG481342
BG386339
BI200064
BE249908
BE267669
BF267625
BF308488
                   BH811443
AW783945
AL710341
BES60457
BQ805991
BEZ64866
BE796178
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BE903091
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BE714855
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                                                                                (without alignments)
11113.872 Million cell updates/sec
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                                                                                                                                 atggcacttgcaccgagcta......gcctggtgccagcagcatag 1929
                                                                      2002, 04:43:45; Search time 2811 Seconds
                                                                                                                                                                                                                          32308132
          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                  16154066 seqs, 8097743376 residues
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                                                 nugleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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em_gss_other:*
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1929
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Maximum DB seq length: 2000000000
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em_estfun:*
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AQ280543 CITBI-EI-BM803905 AGENCOURT B1050480 CM3-GN031 AQ046343 RPCIII-34 AQ697937 HS, 5536\_B AUI33639 AUI33639

AQ280543 BM803905 BI050480 AQ046343 AQ697937 AUI33639

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Result

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Word size :

Database

Searched:

Seguence:

Perfect



FEATURES

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Eukaryotz, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini; Hominidae; Homo. 1 (bases I to 285) to 287 to 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Adult"
./note="Organ: placenta_normal; Vector: puc18; Site_1: Smal : Site_2: Smal; Adult"
./note="Organ: placenta_normal; Vector: puc18; Site_1: Smal : Site_2: Smal; A mini-library was made by cloning products derived from OrgansTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                        BIO50480 285 bp mRNA linear EST 15-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: +55-11-270701
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0313-
050101-59-eo6&t3=2001-01-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence start: 8
High quality sequence start: 8
Location/Qualifiers
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RPCI11-34I18.TK RPCI-11 Homo sapiens genomic clone RPCI-11-34I18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2020263
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/db_xref="taxon:9606"
/clone_lib="GN0313"
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Best Local Similarity 100.0%; P:
.....has 20: Conservative 0;
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AQ046343
AQ046343.1 GI:3315270
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                                                                                                                                                                               BI050480
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                                                                                                                                                                                                                                                 /sex="male"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
calTech Human BAC Library D"
a 192 c 94 g 200 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Gorgan: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. 4 others
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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Pred. No. 0.81;
0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:5520605"
/clone_lib="NIH_MGC_71"
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Location/Qualifiers
                                                                                                                                                                      /db_xref="taxon:9606"
/clone="251406"
/clone_lib="CITBI-E1"
                                                                                    Location/Qualifiers
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100.0%; Pic
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GENERAL INC. 0211934

APPLICANT: Duvick, Jonathan P.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
TITLE OF INVENTION: Polynucleotides and Related Polypeptides of Use
TITLE OF INVENTION: Polynucleotides and Related Polypeptides of Use
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
TITLE OF INVENTION NUMBER: 06/092,936
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 35
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Sequence 35, Application US/09352159A
; Patent No. 6211434
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APPLICANT: Duvick, Jonathan P.
APPLICANT: Duvick, Jacob T.
APPLICANT: Gilliam, Jacob T.
TITLE OF INVENTION: Amino Polyol Amine Oxidase;
TITLE OF INVENTION: Polynucleotides and Relate;
TITLE OF INVENTION: Polynucleotides and Relate;
TITLE OF INVENTION: Polynucleotides and Relate;
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1994-07-12
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
SARLIER FILING DATE: 1999-05-21
NUMBER OF SED ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-352-159-37
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FEATURE:
NAME/KEY: intron
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99.98;
    Query Match
Best Local Similarity 99.9
Matches 1927, Conservative
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Length 1389; Indels

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Sequence 10, Application US/09352159A

Patent No. 6211434

GENERAL INFORMATION:
APPLICANT: DUVICK, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynuclectides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
CURRENT FILINO NUMBER: 60/092,936
FALLER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/135,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/135,391
SAFILER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 1392
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99.7%; Pred. No. 3.3e-159;
tive 0; Mismatches 1;
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OTHER INFORMATION: Extra lysine in K:traPAO
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ORGANISM: Exophiala spinifera
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1389)
NAME/KEY: misc_feature
LOCATION: (1)...(3)
LENGTH: 1389
TYPE: DNA
ORGANISM: Exophiala spinifera
FEATURE:
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Matches 374; Conservative
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                                                                               ) NAME/KEY: CDS
) LOCATION: (1)...(1386)
US-09-352-168-5
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US-09-352-159-10
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GENERAL INFORMATION:
APPLICANT: Crasta, Oswald R.
APPLICANT: Discript, Jonathan P.
APPLICANT: Folkerts, Otto
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Amino Polyol Amine Oxidase
FILE REFERENCE: 0875
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Pred. No. 3.3e-159;
0; Mismatches 1;
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EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
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ORGANISM: Exophiala spinifera
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Best Local Similarity 99.7%;
Matches 374; Conservative
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; LOCATION: (1)...(1386)
US-09-352-159-5
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LENGTH: 1389
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US-09-352-168-5
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Use

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GREERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Duvick, Jose R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynuclectides and Related Polypeptides and Methods of US
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOUTHARE: FASTSEQ for Windows Version 3.0
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Pred. No. 3.3e-159;
0; Mismatches 1;
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ORGANISM: Exophiala spinifera
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Matches 374; Conservative
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US-09-352-159-7
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APPLICANT: O'Sauld R.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Bolister, Otto
APPLICANT: Bolister, Jacob T.
APPLICANT: Maddax, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
TITLE OF INVENTION: Polynucleotides and Related Polypeptides of Use
TITLE OF INVENTION: Polynucleotides and Related Polypeptides of Use
TITLE APPLICATION NUMBER: US/09/352,168A
CURRENT APPLICATION NUMBER: 06/092,936
EARLIER APPLICATION NUMBER: 60/092,936
SARLIER PILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
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  Pred. No. 3.3e-159;
0; Mismatches 1;
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; NAME/KEY: misc_feature
; LOCATION: (1)...(3)
; OTHER INFORMATION: Extra lysine in K:traPAO US-09-352-168-10
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; Sequence 10, Application US/09352168A
; Patent No. 6211435
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ORGANISM: Exophiala spinifera
Best Local Similarity 99.7%;
Matches 374; Conservative
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LOCATION: (1).
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Sequence 20, Application US/09352159A;
Sequence 20, Application US/09352159A;
Patent No. 6211434
GENERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maino Polyol Amine Oxidase
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REPRENCE: 1134
CURRENT APPLICATION NUMBER: 60/092,936
EARLIER PILING DATE: 1998-07-12
EARLIER PILING DATE: 1998-07-25
EARLIER PILING DATE: 1998-07-25
EARLIER FILING DATE: 1998-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARR: FastSEQ for Windows Version 3.0
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1368 TATATGGAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG 1427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Nucleotide sequence of K:trAPAO translational OTHER INFORMATION: fusion with barley alpha amylase signal sequence, OTHER INFORMATION: for expression and secretion of the mature trAPAO OTHER INFORMATION: in maize. Nucleotides 1-72, barley alpha amylase OTHER INFORMATION: signal sequence, nucleotides 73-75, added lysine OTHER INFORMATION: residue; nucleotides 76 -1464 , trAPAO cDNA.

NAME/KEY: sig_peptide
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OTHER INFORMATION: Barley alpha amylase signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.8%; Score 324; DB 4; 99.7%; Pred. No. 3.3e-159;
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0; Mismatches
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COTHER INFORMATION: Added lysine residue US-09-352-159-20
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OTHER INFORMATION: K:traPAOCDNA
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1461)
NAME/KEY: misc_feature
                                      GTGCCAGCAGCATAG 1929
                                                             Best Local Similarity 99.7
Matches 374; Conservative
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NAME/KEY: misc_feature
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ORGANISM: Unknown
                                                                                                                                     RESULT 9
US-09-352-159-20
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                                                           TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG 1914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.36
0; Mismatches
                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09352168A Patent No. 6211435
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ORGANISM: Exophiala spinifera
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Matches 374; Conservative
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NAME/KEY: CDS
LOCATION: (700)...(1439)
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NAME/KEY: intron
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APPLICANT: DUVICK, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
ATTLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polyouclectides and Related Polypeptides and Methods of Use
FILE REPERENCE: 1134
CURRENT APPLICATION NUMBER: 08/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER PILING DATE: 1999-07-25
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                1330 AGAACGCCGTTCAAGAGTGTTCATTTCGTTGGAACGGAGGCGCCTTTAGTTTGGAAAGGG 1389
              1210 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC 1269
                                                                                         1270 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1329
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OTHER INFORMATION: yeast alpha mating factor secretion signal.
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US-09-352-159-16
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LENGTH: 1673
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Best Local S
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| Sequence 20, Application US/09352168A
| Patent No. 6211435
| GENERAL INPORMATION:
| APPLICANT: Crasta, Oswald R.
| APPLICANT: Crasta, Oswald R.
| APPLICANT: DUVICK, Jonathan P.
| APPLICANT: EVINENT:
| APPLICANT: FOILER:
| APPLICANT: Maddox, Joyce R.
| TITLE OF INVENTION: Polyol Amine Oxidase
| TITLE OF INVENTION: Polyol Amine Dolyol Amine Oxidase
| TITLE OF INVENTION: Polyol Amine Polyol Amine Oxidase
| TITLE REFERENCE: 0875
| CURRENT APPLICATION NUMBER: US/09/352,168A
| CURRENT FILING DATE: 1999-07-12
| EARLIER PILING DATE: 1998-07-25
| NUMBER OF SEQ ID NOS: 33
| SOFTWARE: FastSEQ for Windows Version 3.0
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                             1330 AGAACGCCGTTCAAGAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG 1389
                                                                                              1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG 1914
                                                                                                                       1390 IAIAIGAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGGTAAGCCTG 1449
1795 AGAACGCCGTTCAAGTGTGTTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG 1854
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NAME/KEY: CDS.
(1461)
COCATION: (1)...(1461)
OTHER INFORMATION: Nucleotide sequence of K:traPAO translational
OTHER INFORMATION: for expression and secretion of the mature traPAO
OTHER INFORMATION: in maize. Nucleotides 1-72, barley alpha amylase
OTHER INFORMATION: in maize. Nucleotides 1-72, barley alpha amylase
OTHER INFORMATION: signal sequence, nucleotides 775, added lysine
OTHER INFORMATION: residue; nucleotides 76 -1464, traPAO cDNA.
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OTHER INFORMATION: Barley Alpha Amylase signal seguence.
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Pred. No. 3.3e-159;
0; Mismatches 1;
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COTHER INFORMATION: Added lysine residue

US-09-352-168-20
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NAME/KEX: misc_feature

LOCATION: (73)...(1464)

OTHER INFORMATION: K:trapaocbna
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                                                                                                                                                                                         1915 GTGCCAGCAGCATAG 1929
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Best Local Similarity 99.7
Matches 374; Conservative
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US-09-352-168-20
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LENGTH: 1464
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Use

1651 GTGCCAGCAGCATAG 1665

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1531 AGAACGCCGTTCAAGAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG 1590

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DUVICK, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce T.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polyoucleotides and Related Polypeptides and Methods of Use
TITLE OF INVENTION: Polyoucleotides and Related Polypeptides and Methods of Use
TITLE OF INVENTION: Polyoucleotides and Related Polypeptides and Methods of Use
TITLE OF INVENTION: POLYOUCLEOTIDS
CURRENT APPLICATION NUMBER: 05/092,936
EARLIER PEPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
MUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 202
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Pred. No. 3.3e-159;
0; Mismatches 1;
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                                                        ; Sequence 22, Application US/09352159A; Patent No. 6211434
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APPLICANT: Crasta, Oswald R.
APPLICANT: Duvick, Jobathan P.
APPLICANT: Folkerts, Otto
APPLICANT: Gilliam, Jacob T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Exophiala spinifera
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US-09-352-159-22
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Best Local Similarity
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US-09-352-168-22
                  RESULT 13
US-09-352-159-22
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US-09-352-168-16
Sequence 16, Application US/09352168A
Sequence 16, Application US/09352168A
Sequence 16, Application US/09352168A
GENERAL INFORMATION:
APPLICANT: Crasta, Oswald R.
APPLICANT: DUVICK, Jonathan P.
APPLICANT: GIlliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT FILING DATE: 1999-07-12
EARLIER FILING DATE: 1998-07-12
EARLIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
: SOFTWARE: FastSEQ for Windows Version 3.0
: LENGTH: 1673
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                      Gaps
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LOCATION: (1)...(267)
OTHER INFORMATION: yeast alpha mating factor secretion signal.
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16.8%; Score 324; DB 4; I
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1;
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; LOCATION: (1)...(1662)
US-09-352-168-16
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Search completed: November 12, 2002, 07:55:23 Job time : 87 secs
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                                                          NAME/KEY: intron
LOCATION: (739).
    TYPE: DNA ORGANISM: I
                                            FEATURE:
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; Sequence 39, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polyoucleotides and Related Polypeptides and Methods of Use
; TITLE OF INVENTION: NUMBER: US/09/352,159A
; CURRENT APPLICATION NUMBER: 60/092,936
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILLING DATE: 1999-05-21
; BARLIER PLING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 1930
APPLICANT: Maddox, Joyce R.

TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Amino Polyol Amine Oxidase
FITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
EARLIER APPLICATION NUMBER: 06/092,936
EARLIER APPLICATION NUMBER: 06/092,936
EARLIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FactSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 1803
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Pred. No. 3.3e-159;
0; Mismatches 1;
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Best Local Similarity 99.7%;
Matches 374; Conservative
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US-09-352-168-22
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Pred. No. 3.3e-159;
0; Mismatches 1;
; LOCATION: (739)...(811)
; NAME/KEY: intron
; LOCATION: (1134)...(1187)
; NAME/KEY: misc_feature
; LOCATION: (648)...(648)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-159-39
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Best Local Similarity 99.7%;
Matches 374; Conservative (
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Sequence 887, App
Sequence 939, App
Sequence 10314, App
Sequence 7447, App
Sequence 7462, App
Sequence 7464, App
Sequence 7467, App
Sequence 19193, App
Sequence 19193, App
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Sequence 134, App
Sequence 905, App
Sequence 170, App
Sequence 57, Appl
Sequence 3, Appli
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8346.111 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PUS07_BUBCOMB.seq:*
3: /cgn2_6/ptodata/2/pubpna/PUS06_NEW_PUB.seq:*
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7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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8: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-833-263-887

US-09-222-117-939

US-09-22-217-939

US-09-878-574-10314

US-09-878-574-10314

US-09-960-352-7464

US-09-960-352-7464

US-09-960-352-7464

US-09-964-761-2462

US-09-864-761-247

US-09-938-6428-4623

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Sequence 14, Appl Sequence 12039, A Sequence 12494, A Sequence 12759, A Sequence 1815, App Sequence 515, App Sequence 1810, App Sequence 1651, A Sequence 227, App Sequence 227, Ap
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                      Sequence 26,
Sequence 14
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APPLICANT: Botaci, Michael J.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Madgler, Madeleine Joy
APPLICANT: Tongtong
APPLICANT: Tongtong
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471013
CURRENT FILING DAFE: 2001-08-03
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DAFE: 2001-08-03
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 887
LENGTH: 222
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Pred. No. 1.7;
0; Mismatches 0; Indels
                                    US-09-779-233-14
US-09-960-352-12039
US-09-960-352-12494
US-09-960-352-12494
US-09-960-352-12494
US-09-923-876-355-12494
US-09-923-876-515
US-09-923-876-515
US-09-923-876-515
US-09-923-876-515
US-09-920-876-1889
US-09-770-791-845
US-09-770-791-845
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US-09-770-791-889
US-09-770-791-88
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US-09-864-761-29869
US-09-960-352-1982
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-09-867-701-5519
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Patent No. US/0020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Stolk, John A.
APPLICANT: Sinth, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: Mang, Aiun
APPLICANT: Mang, Aiun
APPLICANT: Mang, Aiun
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  Query Match 1.0
Best Local Similarity 100.
Matches 19; Conservative
ORGANISM: Homo sapiens
  RESULT 1
US-09-922-217-887
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US-09-833-263-887
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APPLICANT: Clapper, Jonathan D.
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                               GENERAL INFORMATION:

APPLICANT: Wang, Aijun

APPLICANT: Wang, Aijun

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Madeleine J.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

CURRENT APPLICATION NUMBER: US/09/933,263

CURRENT FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 1093

SOFTWARE PRESEQ FOR WINDOWS Version 3.0

SEQ ID NO 887

LENGTH: 222
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APPLICANT: XU, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secritst, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stilt, John A.
APPLICANT: Stilt, John A.
APPLICANT: Shilt, Carole Lynn
APPLICANT: Shilt, Carole Lynn
APPLICANT: Shilt, Carole Lynn
APPLICANT: Mang, Aijun
APPLICANT: Mang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Mang, Aijun
APPLICANT: Mang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Mang, Aijun
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APPLICANT: Clapper, Jonathan D.
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APPLICANT: Clapper, Jonathan D.
APPLICANT: Mang, Aijun
APPLICANT: Mang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Mang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Mang, Aijun
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Mismatches
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US-09-833-263-939
Sequence 939, Application US/09833263
Fatent No. US20020110547A1
GENERAL INFORMATION:
APPLICANT: Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-09-922-217-939
Sequence 939, Application US/09922217
Patent No. US20020076414A1
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Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
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Best Local Similarity 100.
Matches 19; Conservative
Patent No. US20020110547A1
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US-09-833-263-887
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Sequence 10314, Application US/09878574

Sequence 10314, Application US/09878574

Patent No. US20020110548A1

GENERAL INFORMATION:
APPLICANT: Dayrum, Joseph R.
TATLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: US/09/878,574

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 1999-06-14

PRIOR PEPLICATION NUMBER: 09/333,535

PRIOR FILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

SEQ ID NO 10314
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Patent No. US20020110548A1

GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)8

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR PRILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775
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APPLICANT: Stoik, John A.

PAPLICANT: Madeleine J.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.471C12

CURRENT APPLICATION NUMBER: US/09/833,263

CURRENT FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 939

LENGTH: 228
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23;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Glycine max
COTHER INFORMATION: Clone ID: 701103537H1
US-09-878-574-10314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.9%; Score 17;
                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.0%; Sc
Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1668 CGCCGGGCCCCAAGTCCCA 1686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 CTCAATTACTACATCGT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.99
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                      TYPE: DNA
; ORGANISM: Homo sapien
US-09-833-263-939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-09-878-574-7447
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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 32-LIB3058-049-Q1-K1-H7
US-09-960-352-7464
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APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                        136 GACAAAGTCTGTCTGG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.1
                                                                                                                                                       Conservative
                                                                                                     Query Match
Best Local Similarity
Matches 17; Conserva
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US-09-864-761-2462
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Sequence 1462, Application US/09923876

Patent No. US20020013958A1

SENERAL INPORMATON:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ramigaki, Laura Y. (Ito)
APPLICANT: Ramigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TILE POINVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT APPLICATION NUMBER: U9/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-05-55

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL Program

SEQ ID NO 1462

LENGTH: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
SEQ ID NOS: 15112
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CTHER INFORMATION: Incyte ID No. US20020013958A1 700158849H1

NAME/KEY: unsure

LOCATION: 250, 254, 261, 263

COTRER INFORMATION: a, t, c, g, or other

US-09-923-876-1462
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Pred. No. 23;
0; Mismatches 0; Indels
                                                                                                                                                                          Score 17; DB 10; Length 261;
Pred. No. 23;
0; Mismatches 0; Indels
                                                                                                         CTHER INFORMATION: Clone ID: 701099887H1
US-09-878-574-7447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-960-352-7464
Sequence 7464, Application US/09960352
; Patent No. US/0020137139a1
; GENERAL INFORMATION:
                                                                                                                                                                       Query Match 0.9%; Sox
Best Local Similarity 100.0%; Pi
Matches 17; Conservative 0;
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Best Local Similarity 100.0%; P
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                                                                                                                                                                                                                                                                 232 CTCAATTACTACATCGT 248
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                                                                                                                                                                                                                                                                                      35 CTCAATTACTACATCGT 51
                                                                TYPE: DNA ORGANISM: Glycine max
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ORGANISM: Zea mays
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                    SEQ ID NO 7447
LENGTH: 261
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Sequence 4610, Application US/09960352

Sequence 4610, Application US/09960352

Patent No. US2002013713941

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagapan
APPLICANT: Mathialagan, Nagapan
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC AND FAT DEPOSITION
FILE REPRENCE: 16511.006/37-21(10298)C
FURE REPRENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION DATE: 2001-09-24
SEQ ID NO 4610

FRANCH. A.2
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penh, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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Pred. No. 23;
0; Mismatches 0; Indels
                   Length 433;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA

ORGANISM: Bos taurus

CHER INDERATION: Clone ID: 20-LIB3058-021-Q1-K1-E7

US-09-960-352-4610
                ore 17; DB 10;
red. No. 23;
Mismatches 0
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CURRENT FILING DATE: 2001-05-23
PRIOR PELLOATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-07
PRIOR FILING DATE: 2000-02-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR PLICATION NUMBER: US 60/236,356
PRIOR FILING DATE: 2000-09-04
PRIOR APPLICATION NUMBER: US 60/236,359
                Score 17;
Pred. No.
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APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
0.9%; Scu-
100.0%; Pre
0;
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                                                                                                                     1625 GACAAAGTCTGTCTGG 1641
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X.
CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
OTHER INFORMATION: BXPRESSED IN BRAIN, SIGNAL = 2.1
US-09-864-761-7247
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-30
PRIOR PELING DATE: 2000-09-30
PRIOR PELING DATE: 2000-09-31
PRIOR PELING DATE: 2000-09-30
PRIOR PELING DATE: 2000-09-30
PRIOR PELING DATE: 2001-01-29
PRIOR PELING DATE: 2001-01-29
PRIOR PELING DATE: 2001-01-29
PRIOR PELING DATE: 2000-09-31
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.9%; Scc
Best Local Similarity 100.0%; Pr
Matches 17; Conservative 0;
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Annol
SEQ ID NO 7247
LENGTH: 597
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APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HOMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HOMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HOMBER: US/09/864,761
CURRENT PELLOR DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-05-36
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR PELLORION NUMBER: US 60/207,456
PRIOR PELLORION NUMBER: US 60/207,456
PRIOR PELLORION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-36
PRIOR PELLORION NUMBER: US 60/235,366
PRIOR FILING DATE: 2000-010-04
PRIOR FILING DATE: 2000-010-04
PRIOR FILING DATE: 2000-010-04
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100.0%; Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. EXPRESSED IN HBL100, SIGNAL
N. EXPRESSED IN HELA, SIGNAL = 70
N. EXPRESSED IN HELA, SIGNAL = 70
N. EXPRESSED IN HEARN, SIGNAL = 5.2
N. EXPRESSED IN LUNG, SIGNAL = 5.2
N. EXPRESSED IN BT474, SIGNAL = 25
ON: EXPRESSED IN BT474, SIGNAL = 55
ON: EXPRESSED IN ADULT LIVER, SIGNAL = 70
N. EXPRESSED IN ADULT LIVER = 70
N. EXPRESSED IN ADULT E 70
N. EXPRESSED E 70
N. EXPRESSED E 70
N. EXPRESSED E 70
N. EXP
                                                                             PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO SEQ ID NOS: 49117
SEQ ID NO SEQ ID NOS: 49117
SEQ ID NO 2462
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EXPRESSED IN BAT44, SIGNAL = 55
EXPRESSED IN ADULT LIVER, SIGNAL
EXPRESSED IN PLACENTA, SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. ...
                                    APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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     FILING DATE: 2001-01-30
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Best Local Similarity 100.
Matches 17; Conservative
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ORGANISM: Homo sapiens
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OTHER INFORMATION: BY
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RESULT 14
US-09-938-842A-4623/C
15 Sequence 4623, Application US/09938842A
15 Sepuration INFORMATION:
16 APPLICANT: Harper, Jeff
17 APPLICANT: Harper, Jeff
18 APPLICANT: Wang, Xun
18 APPLICANT: Wang, Xun
18 APPLICANT: SAME, AND METHODS OF USE
17 ITLE OF INVENTION: SAME, AND METHODS OF USE
17 ITLE OF INVENTION: SAME, AND METHODS OF USE
18 ITLE REFERENCE: SCRIP1300-3
19 CURRENT APPLICATION NUMBER: US/09/938,842A
19 PRIOR APPLICATION NUMBER: US 60/227,866
19 PRIOR FILING DATE: 2001-08-24
19 PRIOR FILING DATE: 2001-01-16
19 PRIOR FILING DATE: 2001-06-22
19 NUMBER OF SEQ ID NOS: 5379
19 SEQ ID NO 4623
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APPLICANT: Garcia, Carlos A.
APPLICANT: Slader, Ted
APPLICANT: Date: Ted
APPLICANT: Date: Ted
APPLICANT: Allen, Keith R.
APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILLE OF INVENTION: thallana
FILLE OF INVENTION: Thallana
FILLE OF INVENTION UNMER: US/09/770,445
CURRENT APPLICATION NUMBER: US 60/178,472
PRIOR FILLING DATE: 2000-01-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 999
SOFTWARE. FastSEQ for Windows Version 4.0
SEQ ID NO 714
LENGTH: 826
                                                                                                                         Page, Amy
Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4623
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; ORGANISM: Arabidopsis thaliana
US-09-770-445-714
                           Yu, Yang
Rameaka, Joshua G.
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Matches 17; Conservative
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 12

OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 9.7

OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 70

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 70

OTHER INFORMATION: EXPRESSED IN HERA, SIGNAL = 16

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2

OTHER INFORMATION: EXPRESSED IN BY 44, SIGNAL = 5.5

OTHER INFORMATION: EXPRESSED IN BUTY LIVER, SIGNAL = 5.5

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.3

OTHER INFORMATION: TO THE STANDARD STA
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
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PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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PRIOR PILING DATE: 2000-09-31
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-3
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US-09-770-445-714
US-09-770-445-714
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Matches 17; Conservative
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RESULT 15
US-09-251-134/c
| Sequence 134, Application US/09925301
| Fatent No. US2002052208a1
| Fatent No. US2002052208a1
| Fatent No. US2002052208a1
| GENERAL INFORMATION:
| APPLICARY: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFREENEE: Papel 12001-08-10
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-12
| WUMBER OF EXQ IÓ NOS: 1694
| SEQ ID NO. 134
| LENGTHA: 1657
| TYPE: DNA | ORGANISM: Homo sapiens | O.94; Score 17; DB 10; Length 1657; |
| MACTIVE DATE | O.04; Pred. No. 25; |
| MACTIVE DATE | O.04; Pred. No. 25; |
| MACTIVE DATE | O.04; Pred. No. 25; |
| MACTIVE DATE | O.04; Pred. No. 25; |
| MACTIVE DATE | O.04; Pred. No. 25; |
| MACTIVE DATE | O.04; Pred. No. 25; |
| MACTIVE DATE | O.04; PRED. DATE
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